

SEQUENCE LISTING

5 <110> KUEHN, Ralf
 FELDER, Susanne
 SCHWENK, Frieder
 KUETER-LUKS, Birgit
 FAUST, Nicole

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<213> Artificial Sequence

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25

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25

35

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27

45

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50

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55

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tgtggaagat ccccaggctc ccagcaggc agaagtatgc aaagcatgca tctcaattag 180
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	Thr Gln Arg Ser Ala Asn Glu Asp Lys Ala Ala Asp Leu Gln Arg Glu	
	35 40 45	
0	gtc gag cgc gac ggg ggc cgg ttc agg ttc gtc ggg cat ttc agc gaa	192
	Val Glu Arg Asp Gly Gly Arg Phe Arg Phe Val Gly His Phe Ser Glu	
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	Arg Ile Leu Asn Glu Cys Arg Ala Gly Arg Leu Asn Met Ile Ile Val	
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	Tyr Asp Val Ser Arg Phe Ser Arg Leu Lys Val Met Asp Ala Ile Pro	
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	Ile Val Ser Glu Leu Leu Ala Leu Gly Val Thr Ile Val Ser Thr Gln	
	115 120 125	
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	Glu Gly Val Phe Arg Gln Gly Asn Val Met Asp Leu Ile His Leu Ile	
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	Ile Leu Asp Thr Lys Asn Leu Gln Arg Glu Leu Gly Gly Tyr Val Gly	
	165 170 175	
65	ggg aag gcg cct tac ggc ttc gag ctt gtt tgc gag acg aag gag atc	576
	Gly Lys Ala Pro Tyr Gly Phe Glu Leu Val Ser Glu Thr Lys Glu Ile	
	180 185 190	
70	acg cgc aac ggc cga atg gtc aat gtc gtc atc aac aag ctt gcg cac	624
	Thr Arg Asn Gly Arg Met Val Asn Val Val Ile Asn Lys Leu Ala His	
	195 200 205	
75	tgc acc act ccc ctt acc gga ccc ttc gag ttc gag ccc gac gta atc	672
	Ser Thr Thr Pro Leu Thr Gly Pro Phe Glu Phe Glu Pro Asp Val Ile	

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15	aag cgc atg gac gct gac gcc gtg cgg acc cgg ggc gag acg att ggg Lys Arg Met Asp Ala Asp Ala Val Pro Thr Arg Gly Glu Thr Ile Gly 260 265 270			816
20	aag aag acc gct tca agc gcc tgg gac cgg gca acc gtt atg cga atc Lys Lys Thr Ala Ser Ser Ala Trp Asp Pro Ala Thr Val Met Arg Ile 275 280 285			864
25	ctt cgg gac cgg cgt att gcg ggc ttc gcc gct gag gtg atc tac aag Leu Arg Asp Pro Arg Ile Ala Gly Phe Ala Ala Glu Val Ile Tyr Lys 290 295 300			912
30	aag aag cgg gac ggc acg ccg acc acg aag att gag ggt tac cgc att Lys Lys Pro Asp Gly Thr Pro Thr Thr Lys Ile Glu Gly Tyr Arg Ile 305 310 315 320			960
35	cag cgc gac ccg atc acg ctc cgg ccg gtc gag ctt gat tgc gga ccg Gln Arg Asp Pro Ile Thr Leu Arg Pro Val Glu Leu Asp Cys Gly Pro 325 330 335			1008
40	atc atc gag ccc gct gag tgg tat gag ctt cag gcg tgg ttg gac ggc Ile Ile Glu Pro Ala Glu Trp Tyr Glu Leu Gln Ala Trp Leu Asp Gly 340 345 350			1056
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50	atg gac aag ctg tac tgc gag tgt ggc gcc gtc atg act tgc aag cgc Met Asp Lys Leu Tyr Cys Glu Cys Gly Ala Val Met Thr Ser Lys Arg 370 375 380			1152
55	ggg gaa gaa tgc atc aag gac tct tac cgc tgc cgt cgc cgg aag gtg Gly Glu Glu Ser Ile Lys Asp Ser Tyr Arg Cys Arg Arg Arg Lys Val 385 390 395 400			1200
60	gtc gac ccg tcc gca cct ggg cag cac gaa ggc acg tgc aac gtc agc Val Asp Pro Ser Ala Pro Gly Gln His Glu Gly Thr Cys Asn Val Ser 405 410 415			1248
65	atg gcg gca ctc gac aag ttc gtt gcg gaa cgc atc ttc aac aag atc Met Ala Ala Leu Asp Lys Phe Val Ala Glu Arg Ile Phe Asn Lys Ile 420 425 430			1296
70	agg cac gcc gaa ggc gac gaa gag acg ttg gcg ctt ctg tgg gaa gcc Arg His Ala Glu Gly Asp Glu Glu Thr Leu Ala Leu Leu Trp Glu Ala 435 440 445			1344
75	gcc cga cgc ttc ggc aag ctc act gag gcg cct gag aag agc ggc gaa Ala Arg Arg Phe Gly Lys Leu Thr Glu Ala Pro Glu Lys Ser Gly Glu 450 455 460			1392
80	cgg gcg aac ctt gtt gcg gag cgc gcc gac gcc ctg aac gcc ctt gaa Arg Ala Asn Leu Val Ala Glu Arg Ala Asp Ala Leu Asn Ala Leu Glu 465 470 475 480			1440
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Glu Leu Tyr Glu Asp Arg Ala Ala Gly Ala Tyr Asp Gly Pro Val Gly
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5 agg aag cac ttc cgg aag caa cag gca gcg ctg acg ctc cgg cag caa 1536
 Arg Lys His Phe Arg Lys Gln Gln Ala Ala Leu Thr Leu Arg Gln Gln
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10 ggg gcg gaa gag cgg ctt gcc gaa ctt gaa gcc gcc gaa gcc ccg aag 1584
 Gly Ala Glu Glu Arg Leu Ala Glu Leu Glu Ala Ala Glu Ala Pro Lys
 515 520 525

15 ctt ccc ctt gac caa tgg ttc ccc gaa gac gcc gac gct gac ccg acc 1632
 Leu Pro Leu Asp Gln Trp Phe Pro Glu Asp Ala Asp Ala Asp Pro Thr
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20 ttc gtc ggg ctc ttc gta gac aag atc gtt gtc acg aag tgc act acg 1728
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 565 570 575

25 ggc agg ggg cag gga acg ccc atc gag aag cgc gct tgc atc acg tgg 1776
 Gly Arg Gly Gln Gly Thr Pro Ile Glu Lys Arg Ala Ser Ile Thr Trp
 580 585 590

30 ggc aag ccg ccg acc gac gac gac gaa gac gac gcc cag gac ggc acg 1824
 Ala Lys Pro Pro Thr Asp Asp Asp Glu Asp Asp Ala Gln Asp Gly Thr
 595 600 605

35 gaa gac gta gcg gcg tag 1842
 Glu Asp Val Ala Ala
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50 Thr Gln Arg Ser Ala Asn Glu Asp Lys Ala Ala Asp Leu Gln Arg Glu
 35 40 45

Val Glu Arg Asp Gly Gly Arg Phe Arg Phe Val Gly His Phe Ser Glu
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55 Ala Pro Gly Thr Ser Ala Phe Gly Thr Ala Glu Arg Pro Glu Phe Glu
 65 70 75 80

60 Arg Ile Leu Asn Glu Cys Arg Ala Gly Arg Leu Asn Met Ile Ile Val
 85 90 95

Tyr Asp Val Ser Arg Phe Ser Arg Leu Lys Val Met Asp Ala Ile Pro
 100 105 110

65 Ile Val Ser Glu Leu Leu Ala Leu Gly Val Thr Ile Val Ser Thr Gln
 115 120 125

Glu Gly Val Phe Arg Gln Gly Asn Val Met Asp Leu Ile His Leu Ile

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5	Ile Leu Asp Thr Lys Asn Leu Gln Arg Glu Leu Gly Gly Tyr Val Gly		
	165	170	175
10	Gly Lys Ala Pro Tyr Gly Phe Glu Leu Val Ser Glu Thr Lys Glu Ile		
	180	185	190
	Thr Arg Asn Gly Arg Met Val Asn Val Val Ile Asn Lys Leu Ala His		
	195	200	205
15	Ser Thr Thr Pro Leu Thr Gly Pro Phe Glu Phe Glu Pro Asp Val Ile		
	210	215	220
	Arg Trp Trp Trp Arg Glu Ile Lys Thr His Lys His Leu Pro Phe Lys		
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0	Pro Gly Ser Gln Ala Ala Ile His Pro Gly Ser Ile Thr Gly Leu Cys		
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5	Lys Arg Met Asp Ala Asp Ala Val Pro Thr Arg Gly Glu Thr Ile Gly		
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	Lys Lys Thr Ala Ser Ser Ala Trp Asp Pro Ala Thr Val Met Arg Ile		
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10	Leu Arg Asp Pro Arg Ile Ala Gly Phe Ala Ala Glu Val Ile Tyr Lys		
	290	295	300
	Lys Lys Pro Asp Gly Thr Pro Thr Thr Lys Ile Glu Gly Tyr Arg Ile		
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15	Gln Arg Asp Pro Ile Thr Leu Arg Pro Val Glu Leu Asp Cys Gly Pro		
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40	Ile Ile Glu Pro Ala Glu Trp Tyr Glu Leu Gln Ala Trp Leu Asp Gly		
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	Arg Gly Arg Gly Lys Gly Leu Ser Arg Gly Gln Ala Ile Leu Ser Ala		
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45	Met Asp Lys Leu Tyr Cys Glu Cys Gly Ala Val Met Thr Ser Lys Arg		
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	Gly Glu Glu Ser Ile Lys Asp Ser Tyr Arg Cys Arg Arg Arg Lys Val		
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	Met Ala Ala Leu Asp Lys Phe Val Ala Glu Arg Ile Phe Asn Lys Ile		
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55	Arg His Ala Glu Gly Asp Glu Glu Thr Leu Ala Leu Leu Trp Glu Ala		
	435	440	445
60	Ala Arg Arg Phe Gly Lys Leu Thr Glu Ala Pro Glu Lys Ser Gly Glu		
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	Arg Ala Asn Leu Val Ala Glu Arg Ala Asp Ala Leu Asn Ala Leu Glu		
	465	470	475 480
65	Glu Leu Tyr Glu Asp Arg Ala Ala Gly Ala Tyr Asp Gly Pro Val Gly		
	485	490	495

Arg Lys His Phe Arg Lys Gln Gln Ala Ala Leu Thr Leu Arg Gln Gln
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 5 Gly Ala Glu Glu Arg Leu Ala Glu Leu Glu Ala Ala Glu Ala Pro Lys
 515 520 525
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 530 535 540
 10 Gly Pro Lys Ser Trp Trp Gly Arg Ala Ser Val Asp Asp Lys Arg Val
 545 550 555 560
 Phe Val Gly Leu Phe Val Asp Lys Ile Val Val Thr Lys Ser Thr Thr
 565 570 575
 15 Gly Arg Gly Gln Gly Thr Pro Ile Glu Lys Arg Ala Ser Ile Thr Trp
 580 585 590
 20 Ala Lys Pro Pro Thr Asp Asp Asp Glu Asp Asp Ala Gln Asp Gly Thr
 595 600 605
 Glu Asp Val Ala Ala
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 30 <212> DNA
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 35 coding for fusion protein C31-Int (CNLS)
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 <222> (1)..(1860)
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 Asp Arg Gln Ser Arg Glu Arg Glu Asn Ser Ser Ala Ala Ser Pro Ala
 20 25 30
 50 aca cag cgt agc gcc aac gaa gac aag gcg gcc gac ctt cag cgc gaa 144
 Thr Gln Arg Ser Ala Asn Glu Asp Lys Ala Ala Asp Leu Gln Arg Glu
 35 40 45
 55 gtc gag cgc gac ggg ggc cgg ttc agg ttc gtc ggg cat ttc agc gaa 192
 Val Glu Arg Asp Gly Gly Arg Phe Arg Phe Val Gly His Phe Ser Glu
 50 55 60
 gcg ccg ggc acg tcg gcg ttc ggg acg gcg gag cgc ccg gag ttc gaa 240
 Ala Pro Gly Thr Ser Ala Phe Gly Thr Ala Glu Arg Pro Glu Phe Glu
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 Arg Ile Leu Asn Glu Cys Arg Ala Gly Arg Leu Asn Met Ile Ile Val
 85 90 95
 65 tat gac gtg tcg cgc ttc tcg cgc ctg aag gtc atg gac gcg att ccg 336
 Tyr Asp Val Ser Arg Phe Ser Arg Leu Lys Val Met Asp Ala Ile Pro

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10	gaa ggc gtc ttc cgg cag gga aac gtc atg gac ctg att cac ctg att Glu Gly Val Phe Arg Gln Gly Asn Val Met Asp Leu Ile His Leu Ile 130 135 140			432
15	atg cgg ctc gac gcg tcg cac aaa gaa tct tcg ctg aag tcg gcg aag Met Arg Leu Asp Ala Ser His Lys Glu Ser Ser Leu Lys Ser Ala Lys 145 150 155 160			480
20	att ctc gac acg aag aac ctt cag cgc gaa ttg ggc ggg tac gtc ggc Ile Leu Asp Thr Lys Asn Leu Gln Arg Glu Leu Gly Gly Tyr Val Gly 165 170 175			528
25	ggg aag gcg cct tac ggc ttc gag ctt gtt tcg gag acg aag gag atc Gly Lys Ala Pro Tyr Gly Phe Glu Leu Val Ser Glu Thr Lys Glu Ile 180 185 190			576
30	acg cgc aac ggc cga atg gtc aat gtc gtc atc aac aag ctt gcg cac Thr Arg Asn Gly Arg Met Val Asn Val Val Ile Asn Lys Leu Ala His 195 200 205			624
35	tcg acc act ccc ctt acc gga ccc ttc gag ttc gag ccc gac gta atc Ser Thr Thr Pro Leu Thr Gly Pro Phe Glu Phe Glu Pro Asp Val Ile 210 215 220			672
40	cgg tgg tgg tgg cgt gag atc aag acg cac aaa cac ctt ccc ttc aag Arg Trp Trp Trp Arg Glu Ile Lys Thr His Lys His Leu Pro Phe Lys 225 230 235 240			720
45	ccg ggc agt caa gcc gcc att cac ccg ggc agc atc acg ggg ctt tgt Pro Gly Ser Gln Ala Ala Ile His Pro Gly Ser Ile Thr Gly Leu Cys 245 250 255			768
50	aag cgc atg gac gct gac gcc gtg ccg acc ccg ggc gag acg att ggg Lys Arg Met Asp Ala Asp Ala Val Pro Thr Arg Gly Glu Thr Ile Gly 260 265 270			816
55	aag aag acc gct tca agc gcc tgg gac ccg gca acc gtt atg cga atc Lys Lys Thr Ala Ser Ser Ala Trp Asp Pro Ala Thr Val Met Arg Ile 275 280 285			864
60	ctt cgg gac ccg cgt att gcg ggc ttc gcc gct gag gtg atc tac aag Leu Arg Asp Pro Arg Ile Ala Gly Phe Ala Ala Glu Val Ile Tyr Lys 290 295 300			912
65	aag aag ccg gac ggc acg ccg acc acg aag att gag ggt tac cgc att Lys Lys Pro Asp Gly Thr Pro Thr Thr Lys Ile Glu Gly Tyr Arg Ile 305 310 315 320			960
70	cag cgc gac ccg atc acg ctc ccg ccg gtc gag ctt gat tgc gga ccg Gln Arg Asp Pro Ile Thr Leu Arg Pro Val Glu Leu Asp Cys Gly Pro 325 330 335			1008
75	atc atc gag ccc gct gag tgg tat gag ctt cag gcg tgg ttg gac ggc Ile Ile Glu Pro Ala Glu Trp Tyr Glu Leu Gln Ala Trp Leu Asp Gly 340 345 350			1056
80	agg ggg cgc ggc aag ggg ctt tcc ccg ggg caa gcc att ctg tcc gcc Arg Gly Arg Gly Lys Gly Leu Ser Arg Gly Gln Ala Ile Leu Ser Ala 355 360 365			1104
85	atg gac aag ctg tac tgc gag tgt ggc gcc gtc atg act tcg aag cgc			1152

<213> Artificial Sequence

<223> Description of Artificial Sequence: DNA sequence
coding for fusion protein C31-Int (CNLS)

5 <400> 23
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1 5 10 15

10 Asp Arg Gln Ser Arg Glu Arg Glu Asn Ser Ser Ala Ala Ser Pro Ala
20 25 30

Thr Gln Arg Ser Ala Asn Glu Asp Lys Ala Ala Asp Leu Gln Arg Glu
35 40 45

15 Val Glu Arg Asp Gly Gly Arg Phe Arg Phe Val Gly His Phe Ser Glu
50 55 60

Ala Pro Gly Thr Ser Ala Phe Gly Thr Ala Glu Arg Pro Glu Phe Glu
65 70 75 80

20 Arg Ile Leu Asn Glu Cys Arg Ala Gly Arg Leu Asn Met Ile Ile Val
85 90 95

25 Tyr Asp Val Ser Arg Phe Ser Arg Leu Lys Val Met Asp Ala Ile Pro
100 105 110

Ile Val Ser Glu Leu Leu Ala Leu Gly Val Thr Ile Val Ser Thr Gln
115 120 125

30 Glu Gly Val Phe Arg Gln Gly Asn Val Met Asp Leu Ile His Leu Ile
130 135 140

Met Arg Leu Asp Ala Ser His Lys Glu Ser Ser Leu Lys Ser Ala Lys
145 150 155 160

35 Ile Leu Asp Thr Lys Asn Leu Gln Arg Glu Leu Gly Gly Tyr Val Gly
165 170 175

40 Gly Lys Ala Pro Tyr Gly Phe Glu Leu Val Ser Glu Thr Lys Glu Ile
180 185 190

Thr Arg Asn Gly Arg Met Val Asn Val Val Ile Asn Lys Leu Ala His
195 200 205

45 Ser Thr Thr Pro Leu Thr Gly Pro Phe Glu Phe Glu Pro Asp Val Ile
210 215 220

Arg Trp Trp Trp Arg Glu Ile Lys Thr His Lys His Leu Pro Phe Lys
225 230 235 240

50 Pro Gly Ser Gln Ala Ala Ile His Pro Gly Ser Ile Thr Gly Leu Cys
245 250 255

Lys Arg Met Asp Ala Asp Ala Val Pro Thr Arg Gly Glu Thr Ile Gly
260 265 270

Lys Lys Thr Ala Ser Ser Ala Trp Asp Pro Ala Thr Val Met Arg Ile
275 280 285

60 Leu Arg Asp Pro Arg Ile Ala Gly Phe Ala Ala Glu Val Ile Tyr Lys
290 295 300

Lys Lys Pro Asp Gly Thr Pro Thr Thr Lys Ile Glu Gly Tyr Arg Ile
305 310 315 320

65 Gln Arg Asp Pro Ile Thr Leu Arg Pro Val Glu Leu Asp Cys Gly Pro
325 330 335

Ile Ile Glu Pro Ala Glu Trp Tyr Glu Leu Gln Ala Trp Leu Asp Gly
 340 345 350
 5 Arg Gly Arg Gly Lys Gly Leu Ser Arg Gly Gln Ala Ile Leu Ser Ala
 355 360 365
 Met Asp Lys Leu Tyr Cys Glu Cys Gly Ala Val Met Thr Ser Lys Arg
 370 375 380
 10 Gly Glu Glu Ser Ile Lys Asp Ser Tyr Arg Cys Arg Arg Arg Lys Val
 385 390 395 400
 15 Val Asp Pro Ser Ala Pro Gly Gln His Glu Gly Thr Cys Asn Val Ser
 405 410 415
 Met Ala Ala Leu Asp Lys Phe Val Ala Glu Arg Ile Phe Asn Lys Ile
 420 425 430
 20 Arg His Ala Glu Gly Asp Glu Glu Thr Leu Ala Leu Leu Trp Glu Ala
 435 440 445
 Ala Arg Arg Phe Gly Lys Leu Thr Glu Ala Pro Glu Lys Ser Gly Glu
 450 455 460
 25 Arg Ala Asn Leu Val Ala Glu Arg Ala Asp Ala Leu Asn Ala Leu Glu
 465 470 475 480
 30 Glu Leu Tyr Glu Asp Arg Ala Ala Gly Ala Tyr Asp Gly Pro Val Gly
 485 490 495
 Arg Lys His Phe Arg Lys Gln Gln Ala Ala Leu Thr Leu Arg Gln Gln
 500 505 510
 35 Gly Ala Glu Glu Arg Leu Ala Glu Leu Glu Ala Ala Glu Ala Pro Lys
 515 520 525
 Leu Pro Leu Asp Gln Trp Phe Pro Glu Asp Ala Asp Ala Asp Pro Thr
 530 535 540
 40 Gly Pro Lys Ser Trp Trp Gly Arg Ala Ser Val Asp Asp Lys Arg Val
 545 550 555 560
 45 Phe Val Gly Leu Phe Val Asp Lys Ile Val Val Thr Lys Ser Thr Thr
 565 570 575
 Gly Arg Gly Gln Gly Thr Pro Ile Glu Lys Arg Ala Ser Ile Thr Trp
 580 585 590
 50 Ala Lys Pro Pro Thr Asp Asp Asp Glu Asp Asp Ala Gln Asp Gly Thr
 595 600 605
 Glu Asp Val Ala Ala Pro Lys Lys Lys Arg Lys Val
 610 615 620
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 <210> 24
 <211> 43
 60 <212> PRT
 <213> Artificial Sequence
 <220>
 <223> Description of Artificial Sequence: NLS
 65
 <400> 24
 Met Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Cys Arg Leu Lys

Lys Leu Lys Cys Ser Lys Glu Lys Pro Lys Cys Ala Lys Cys Leu Lys
20 25 30

5

10

15

0

5

30

35

40

45

50

55

60

65.

 $\langle 220 \rangle$

Pro Lys Lys Ala Arg Glu Asp Val Ser Arg Lys Arg Pro Arg
1 5 10

Ala Pro Lys Arg Lys Ser Gly Val Ser Lys Cys
1 5 10

Glu Glu Asp Gly Pro Gln Lys Lys Lys Arg Arg Leu
1 5 10

Ala Pro Thr Lys Arg Lys Gly Ser
1 5

Pro Asn Lys Lys Lys Arg Lys
1 5

<223> Description of Artificial Sequence: NLS

<400> 34
Lys Arg Pro Arg Pro
1 5

5

<210> 35
<211> 11
<212> PRT
<213> Artificial Sequence

10

<220>
<223> Description of Artificial Sequence: NLS

<400> 35
15 Cys Gly Gly Leu Ser Ser Lys Arg Pro Arg Pro
1 5 10

0

<210> 36
<211> 19
<212> PRT
<213> Artificial Sequence

5

<220>
<223> Description of Artificial Sequence: NLS

<400> 36
Pro Pro Lys Lys Arg Met Arg Arg Arg Ile Glu Pro Lys Lys Lys Lys
1 5 10 15

0

Lys Arg Pro

5

<210> 37
<211> 11
<212> PRT
<213> Artificial Sequence

40

<220>
<223> Description of Artificial Sequence: NLS

<400> 37
45 Pro Phe Leu Asp Arg Leu Arg Arg Asp Gln Lys
1 5 10

50

<210> 38
<211> 9
<212> PRT
<213> Artificial Sequence

55

<220>
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<400> 38
Pro Lys Gln Lys Arg Lys Met Ala Arg
1 5

60

<210> 39
<211> 9
<212> PRT
<213> Artificial Sequence

65

<220>
<223> Description of Artificial Sequence: NLS

<400> 39
 Ser Val Thr Lys Lys Arg Lys Leu Glu
 1 5
 5

<210> 40
 <211> 11
 <212> PRT
 10 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: NLS

15 <400> 40
 Cys Gly Gly Ala Ala Lys Arg Val Lys Leu Asp
 1 5 10

0 <210> 41
 <211> 9
 <212> PRT
 <213> Artificial Sequence

5 <220>
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0 <400> 41
 Pro Ala Ala Lys Arg Val Lys Leu Asp
 1 5

5 <210> 42
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 <213> Artificial Sequence

40 <220>
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<400> 42
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 1 5 10

45 <210> 43
 <211> 8
 <212> PRT
 <213> Artificial Sequence

50 <220>
 <223> Description of Artificial Sequence: NLS

55 <400> 43
 Pro Gln Ser Arg Lys Lys Leu Arg
 1 5

60 <210> 44
 <211> 8
 <212> PRT
 <213> Artificial Sequence

65 <220>
 <223> Description of Artificial Sequence: NLS

<400> 44

Pro Leu Leu Lys Lys Ile Lys Gln
1 5

5 <210> 45
<211> 7
<212> PRT
<213> Artificial Sequence

10 <220>
<223> Description of Artificial Sequence: NLS

<400> 45
Pro Gln Pro Lys Lys Lys Pro
15 1 5

<210> 46
<211> 9
0 <212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: NLS

5 <400> 46
Ser Lys Arg Val Ala Lys Arg Lys Leu
1 5

10 <210> 47
<211> 9
<212> PRT
<213> Artificial Sequence

35 <220>
<223> Description of Artificial Sequence: NLS

<400> 47
40 Ala Ser Lys Ser Arg Lys Arg Lys Leu
1 5

45 <210> 48
<211> 16
<212> PRT
<213> Artificial Sequence

50 <220>
<223> Description of Artificial Sequence: NLS

<400> 48
Gly Gly Leu Cys Ser Ala Arg Leu His Arg His Ala Leu Leu Ala Thr
55 1 5 10 15

<210> 49
<211> 8
<212> PRT
60 <213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: NLS

65 <400> 49
Arg Lys Thr Lys Lys Lys Ile Lys
1 5

5 <210> 50
 <211> 8
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: NLS
 10
 <400> 50
 Arg Lys Leu Lys Lys Leu Gly Asn
 1 5
 15
 <210> 51
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 <212> PRT
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 20
 <220>
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 <400> 51
 25 Arg Lys Asp Arg Arg Gly Gly Arg
 1 5
 30
 <210> 52
 <211> 18
 <212> PRT
 <213> Artificial Sequence
 <220>
 35 <223> Description of Artificial Sequence: NLS
 <400> 52
 Asp Thr Arg Glu Lys Lys Lys Phe Leu Lys Arg Arg Leu Leu Arg Leu
 1 5 10 15
 40
 Asp Glu
 45
 <210> 53
 <211> 7
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 50
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 <400> 53
 55 Pro Lys Lys Lys Arg Lys Val
 1 5
 60
 <210> 54
 <211> 1410
 <212> DNA
 <213> Bacteriophage R4
 <220>
 <221> CDS
 65 <222> (1)..(1407)
 <400> 54

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	Met Asn Arg Gly Gly Pro Thr Val Arg Ala Asp Ile Tyr Val Arg Ile	
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5	agc ctg gac cgc aca ggg gaa gag ctc ggg gtc gag cgc cag gag gag	96
	Ser Leu Asp Arg Thr Gly Glu Glu Leu Gly Val Glu Arg Gln Glu Glu	
	20 25 30	
10	tcg tgt cgc gag ctc tgc aag agc ctc ggc atg gag gtg ggg cag gtg	144
	Ser Cys Arg Glu Leu Cys Lys Ser Leu Gly Met Glu Val Gly Gln Val	
	35 40 45	
15	tgg gtc gac aac gac ctg agc gcc acc aag aag aac gtc gtc cgc cct	192
	Trp Val Asp Asn Asp Leu Ser Ala Thr Lys Lys Asn Val Val Arg Pro	
	50 55 60	
	gac ttc gag gcg atg atc gcg agc aac ccg cag gcg atc gtc tgc tgg	240
	Asp Phe Glu Ala Met Ile Ala Ser Asn Pro Gln Ala Ile Val Cys Trp	
	65 70 75 80	
	cac acc gac cgg ctc atc cgc gtc acg cgg gac ctg gag cgg gtg atc	288
	His Thr Asp Arg Leu Ile Arg Val Thr Arg Asp Leu Glu Arg Val Ile	
	85 90 95	
5	gac ctc gga gtc aac gtc cac gcc gtg atg gcc gga cac ctg gac ctg	336
	Asp Leu Gly Val Asn Val His Ala Val Met Ala Gly His Leu Asp Leu	
	100 105 110	
10	tcc acc ccg gcc ggc cga gcc gtc gcc cgc acg gtg acg gcc tgg gcc	384
	Ser Thr Pro Ala Gly Arg Ala Val Ala Arg Thr Val Thr Ala Trp Ala	
	115 120 125	
35	acg tac gag ggc gag cag aag gct gag cgc cag aag ctc gcc aac atc	432
	Thr Tyr Glu Gly Glu Gln Lys Ala Glu Arg Gln Lys Leu Ala Asn Ile	
	130 135 140	
40	cag aac gcc cgc gcc ggc aag ccg tac acc ccc ggc atc cgc ccc ttc	480
	Gln Asn Ala Arg Ala Gly Lys Pro Tyr Thr Pro Gly Ile Arg Pro Phe	
	145 150 155 160	
	ggg tac ggc gac gac cac atg acc atc gtg acg gcc gag gcg gac gcc	528
	Gly Tyr Gly Asp His Met Thr Ile Val Thr Ala Glu Ala Asp Ala	
	165 170 175	
45	atc cgc gac ggc gcg aag atg atc ctc gac ggc tgg tcc ctg tcg gcc	576
	Ile Arg Asp Gly Ala Lys Met Ile Leu Asp Gly Trp Ser Leu Ser Ala	
	180 185 190	
50	gtg gct cgc tac tgg gag gag ctc aag ctc cag tcg ccc cgg agt atg	624
	Val Ala Arg Tyr Trp Glu Glu Leu Lys Leu Gln Ser Pro Arg Ser Met	
	195 200 205	
55	gcc gca ggc ggc aag ggc tgg tct ctg cgg ggc gta aag aag gtg ctg	672
	Ala Ala Gly Gly Lys Gly Trp Ser Leu Arg Gly Val Lys Lys Val Leu	
	210 215 220	
60	acc tcc ccg cgc tac gtc ggg cgg tcc agc tac ctc ggg gag gtc gtg	720
	Thr Ser Pro Arg Tyr Val Gly Arg Ser Ser Tyr Leu Gly Glu Val Val	
	225 230 235 240	
	ggc gat gct cag tgg ccg ccc atc ctc gac ccg gac gtc tac tac ggg	768
	Gly Asp Ala Gln Trp Pro Pro Ile Leu Asp Pro Asp Val Tyr Tyr Gly	
	245 250 255	
65	gtc gtg gcc atc ctg aac aac ccc gac cgc ttc agc ggg ggc cct cgg	816
	Val Val Ala Ile Leu Asn Asn Pro Asp Arg Phe Ser Gly Gly Pro Arg	
	260 265 270	

acc ggc cgc acc ccc ggc acg ctg ctc gca ggc atc gcc ttg tgc ggt 864
 Thr Gly Arg Thr Pro Gly Thr Leu Leu Ala Gly Ile Ala Leu Cys Gly
 275 280 285

5 gag tgc ggc aag acg gtc agt gga cgc ggc tac cga ggt gtc ctg gtc 912
 Glu Cys Gly Lys Thr Val Ser Gly Arg Gly Tyr Arg Gly Val Leu Val
 290 295 300

10 tac gga tgt aag gac acg cac act cgg acg cct cgg agc atc gct gac 960
 Tyr Gly Cys Lys Asp Thr His Thr Arg Thr Pro Arg Ser Ile Ala Asp
 305 310 315 320

15 ggc cgc ggc agc agc tgc acc ctc gcc cgg ctc atg ttc ccc gac ttc 1008
 Gly Arg Ala Ser Ser Ser Thr Leu Ala Arg Leu Met Phe Pro Asp Phe
 325 330 335

ctg ccc ggc ctc ctg gcc tct ggg cag gcc gag gac ggc cag tgc gca 1056
 Leu Pro Gly Leu Leu Ala Ser Gly Gln Ala Glu Asp Gly Gln Ser Ala
 340 345 350

gca tcc aag cac tgc gag gcc cag acg ctg cgc gag cgc ctt gac ggg 1104
 Ala Ser Lys His Ser Glu Ala Gln Thr Leu Arg Glu Arg Leu Asp Gly
 355 360 365

5 ctg gct acg gcc tac gcg gag ggt gcg atc agc ctg tct cag atg acg 1152
 Leu Ala Thr Ala Tyr Ala Glu Gly Ala Ile Ser Leu Ser Gln Met Thr
 370 375 380

10 gcc ggc tgc gaa gca ctg cgg aag aag ctg gag gtg atc gaa gcc gac 1200
 Ala Gly Ser Glu Ala Leu Arg Lys Lys Leu Glu Val Ile Glu Ala Asp
 385 390 395 400

35 ctc gtg ggc tgc gca ggc atc ccg ccc ttc gat cca gtg gcc gga gtg 1248
 Leu Val Gly Ser Ala Gly Ile Pro Pro Phe Asp Pro Val Ala Gly Val
 405 410 415

40 gct ggc ctg atc tcc ggc tgg ccc acc acg cct ctc ccg acg cgt cga 1296
 Ala Gly Leu Ile Ser Gly Trp Pro Thr Thr Pro Leu Pro Thr Arg Arg
 420 425 430

gca tgg gtg gac ttc tgc ctg gtg gtc acg ctg aac acc cag aag ggg 1344
 Ala Trp Val Asp Phe Cys Leu Val Val Thr Leu Asn Thr Gln Lys Gly
 435 440 445

45 cgc cat gcg tgc agc atg acc gtg gac gac cac gtc acc atc gag tgg 1392
 Arg His Ala Ser Ser Met Thr Val Asp Asp His Val Thr Ile Glu Trp
 450 455 460

50 cga gac gtg gcc gag tag 1410
 Arg Asp Val Ala Glu
 465

55 <210> 55
 <211> 469
 <212> PRT
 <213> Bacteriophage R4

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65 Ser Leu Asp Arg Thr Gly Glu Glu Leu Gly Val Glu Arg Gln Glu Glu
 20 25 30

Ser Cys Arg Glu Leu Cys Lys Ser Leu Gly Met Glu Val Gly Gln Val

	35	40	45
	Trp Val Asp Asn Asp Leu Ser Ala Thr Lys Lys Asn Val Val Arg Pro		
5	50	55	60
	Asp Phe Glu Ala Met Ile Ala Ser Asn Pro Gln Ala Ile Val Cys Trp		
	65	70	75
10	His Thr Asp Arg Leu Ile Arg Val Thr Arg Asp Leu Glu Arg Val Ile		
	85	90	95
	Asp Leu Gly Val Asn Val His Ala Val Met Ala Gly His Leu Asp Leu		
	100	105	110
15	Ser Thr Pro Ala Gly Arg Ala Val Ala Arg Thr Val Thr Ala Trp Ala		
	115	120	125
	Thr Tyr Glu Gly Glu Gln Lys Ala Glu Arg Gln Lys Leu Ala Asn Ile		
	130	135	140
0	Gln Asn Ala Arg Ala Gly Lys Pro Tyr Thr Pro Gly Ile Arg Pro Phe		
	145	150	155
5	Gly Tyr Gly Asp Asp His Met Thr Ile Val Thr Ala Glu Ala Asp Ala		
	165	170	175
	Ile Arg Asp Gly Ala Lys Met Ile Leu Asp Gly Trp Ser Leu Ser Ala		
	180	185	190
30	Val Ala Arg Tyr Trp Glu Glu Leu Lys Leu Gln Ser Pro Arg Ser Met		
	195	200	205
	Ala Ala Gly Gly Lys Gly Trp Ser Leu Arg Gly Val Lys Lys Val Leu		
	210	215	220
35	Thr Ser Pro Arg Tyr Val Gly Arg Ser Ser Tyr Leu Gly Glu Val Val		
	225	230	235
	Gly Asp Ala Gln Trp Pro Pro Ile Leu Asp Pro Asp Val Tyr Tyr Gly		
	245	250	255
40	Val Val Ala Ile Leu Asn Asn Pro Asp Arg Phe Ser Gly Gly Pro Arg		
	260	265	270
45	Thr Gly Arg Thr Pro Gly Thr Leu Leu Ala Gly Ile Ala Leu Cys Gly		
	275	280	285
	Glu Cys Gly Lys Thr Val Ser Gly Arg Gly Tyr Arg Gly Val Leu Val		
	290	295	300
50	Tyr Gly Cys Lys Asp Thr His Thr Arg Thr Pro Arg Ser Ile Ala Asp		
	305	310	315
	Gly Arg Ala Ser Ser Ser Thr Leu Ala Arg Leu Met Phe Pro Asp Phe		
	325	330	335
55	Leu Pro Gly Leu Leu Ala Ser Gly Gln Ala Glu Asp Gly Gln Ser Ala		
	340	345	350
60	Ala Ser Lys His Ser Glu Ala Gln Thr Leu Arg Glu Arg Leu Asp Gly		
	355	360	365
	Leu Ala Thr Ala Tyr Ala Glu Gly Ala Ile Ser Leu Ser Gln Met Thr		
	370	375	380
65	Ala Gly Ser Glu Ala Leu Arg Lys Lys Leu Glu Val Ile Glu Ala Asp		
	385	390	395
			400

Leu Val Gly Ser Ala Gly Ile Pro Pro Phe Asp Pro Val Ala Gly Val
 405 410 415
 5 Ala Gly Leu Ile Ser Gly Trp Pro Thr Thr Pro Leu Pro Thr Arg Arg
 420 425 430
 Ala Trp Val Asp Phe Cys Leu Val Val Thr Leu Asn Thr Gln Lys Gly
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 Arg Asp Val Ala Glu
 15 465
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 20 <211> 1503
 <212> DNA
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 25 <221> CDS
 <222> (1)..(1500)
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 gga tcg agc atc gac agc caa atc gag gcc tgt ata aag aaa gca ggg 96
 Gly Ser Ser Ile Asp Ser Gln Ile Glu Ala Cys Ile Lys Lys Ala Gly
 35 20 25 30
 act aaa gat gtg ctg aag tat gca gat gaa gga ttt tca gga gag ctt 144
 Thr Lys Asp Val Leu Lys Tyr Ala Asp Glu Gly Phe Ser Gly Glu Leu
 35 40 45
 40 tta gaa cgt ccg gct ttg aat cgc ttg agg gag gat gca agc aag gga 192
 Leu Glu Arg Pro Ala Leu Asn Arg Leu Arg Glu Asp Ala Ser Lys Gly
 50 55 60
 45 ctt ata agt caa gtc att tgt tac gat cct gac cgt ctt tct cgg aaa 240
 Leu Ile Ser Gln Val Ile Cys Tyr Asp Pro Asp Arg Leu Ser Arg Lys
 65 70 75 80
 tta atg aat cag cta atc att gat gac gaa ttg cga aag cga aac ata 288
 Leu Met Asn Gln Leu Ile Ile Asp Asp Glu Leu Arg Lys Arg Asn Ile
 85 90 95
 cct ttg att ttt gta aat ggt gaa tac gcc aat tct cca gaa ggt caa 336
 Pro Leu Ile Phe Val Asn Gly Glu Tyr Ala Asn Ser Pro Glu Gly Gln
 100 105 110
 55 ttg ttt ttc gca atg cgc ggg gca atc tca gaa ttt gaa aaa gcc aaa 384
 Leu Phe Phe Ala Met Arg Gly Ala Ile Ser Glu Phe Glu Lys Ala Lys
 115 120 125
 60 atc aaa gaa cgg aca tca agc ggc cga ctt caa aaa atg aaa aaa ggc 432
 Ile Lys Glu Arg Thr Ser Ser Gly Arg Leu Gln Lys Met Lys Lys Gly
 130 135 140
 65 atg atc att aaa gat tct aaa cta tat ggc tat aaa ttt gtt aaa gag 480
 Met Ile Ile Lys Asp Ser Lys Leu Tyr Gly Tyr Lys Phe Val Lys Glu
 145 150 155 160

	aaa	aga	act	ctt	gag	ata	tta	gaa	gag	gaa	gca	aaa	atc	att	cgg	atg	528
	Lys	Arg	Thr	Leu	Glu	Ile	Leu	Glu	Glu	Glu	Ala	Lys	Ile	Ile	Arg	Met	
					165					170					175		
5	att	ttt	aac	tat	ttc	acc	gat	cat	aaa	agc	cct	ttt	ttc	ggc	aga	gta	576
	Ile	Phe	Asn	Tyr	Phe	Thr	Asp	His	Lys	Ser	Pro	Phe	Phe	Gly	Arg	Val	
				180					185					190			
10	aat	ggt	att	gct	cta	cat	tta	act	cag	atg	ggg	gtt	aaa	aca	aaa	aaa	624
	Asn	Gly	Ile	Ala	Leu	His	Leu	Thr	Gln	Met	Gly	Val	Lys	Thr	Lys	Lys	
				195				200					205				
15	ggc	gcc	aaa	gta	tgg	cac	agg	cag	gtt	gtt	cgg	caa	ata	tta	atg	aac	672
	Gly	Ala	Lys	Val	Trp	His	Arg	Gln	Val	Val	Arg	Gln	Ile	Leu	Met	Asn	
		210					215					220					
20	tct	tcc	tat	aag	ggt	gaa	cat	aga	cag	tat	aaa	tat	gat	aca	gag	ggt	720
	Ser	Ser	Tyr	Lys	Gly	Glu	His	Arg	Gln	Tyr	Lys	Tyr	Asp	Thr	Glu	Gly	
	225					230					235					240	
25	tcc	tat	gtt	tca	aag	cag	gca	ggg	aac	aaa	tct	ata	att	aaa	ata	agg	768
	Ser	Tyr	Val	Ser	Lys	Gln	Ala	Gly	Asn	Lys	Ser	Ile	Ile	Lys	Ile	Arg	
					245				250						255		
30	cct	gaa	gaa	gaa	caa	atc	act	gtg	aca	att	cca	gca	att	gtt	cca	gct	816
	Pro	Glu	Glu	Glu	Gln	Ile	Thr	Val	Thr	Ile	Pro	Ala	Ile	Val	Pro	Ala	
				260				265						270			
35	gaa	caa	tgg	gat	tat	gct	caa	gaa	ctc	tta	ggt	caa	agt	aaa	aga	aaa	864
	Glu	Gln	Trp	Asp	Tyr	Ala	Gln	Glu	Leu	Leu	Gly	Gln	Ser	Lys	Arg	Lys	
			275					280					285				
40	cac	ttg	agt	atc	agc	cct	cac	aat	tac	ttg	tta	tcg	ggg	ttg	gtt	aga	912
	His	Leu	Ser	Ile	Ser	Pro	His	Asn	Tyr	Leu	Leu	Ser	Gly	Leu	Val	Arg	
		290					295					300					
45	tgc	gga	aaa	tgc	gga	aat	acc	atg	aca	ggg	aag	aaa	aga	aaa	tca	cat	960
	Cys	Gly	Lys	Cys	Gly	Asn	Thr	Met	Thr	Gly	Lys	Lys	Arg	Lys	Ser	His	
	305					310					315					320	
50	ggt	aaa	gac	tac	tat	gta	tat	act	tgc	cgg	aaa	aat	tat	tct	ggc	gca	1008
	Gly	Lys	Asp	Tyr	Tyr	Val	Tyr	Thr	Cys	Arg	Lys	Asn	Tyr	Ser	Gly	Ala	
					325					330					335		
55	aag	gac	cgc	ggc	tgc	gga	aaa	gaa	atg	tct	gag	aat	aaa	ttg	aac	cgg	1056
	Lys	Asp	Arg	Gly	Cys	Gly	Lys	Glu	Met	Ser	Glu	Asn	Lys	Leu	Asn	Arg	
				340					345					350			
60	cat	gta	tgg	ggt	gaa	att	ttt	aaa	ttc	atc	aca	aat	cct	caa	aag	tat	1104
	His	Val	Trp	Gly	Glu	Ile	Phe	Lys	Phe	Ile	Thr	Asn	Pro	Gln	Lys	Tyr	
			355					360					365				
65	gtt	tct	ttt	aaa	gag	gct	gaa	caa	tca	aat	cac	ctg	tct	gat	gaa	tta	1152
	Val	Ser	Phe	Lys	Glu	Ala	Glu	Gln	Ser	Asn	His	Leu	Ser	Asp	Glu	Leu	
			370				375					380					
70	gaa	ctt	att	gaa	aaa	gag	ata	gag	aaa	aca	aaa	aaa	ggc	cgc	aag	cgt	1200
	Glu	Leu	Ile	Glu	Lys	Glu	Ile	Glu	Lys	Thr	Lys	Lys	Gly	Arg	Lys	Arg	
	385					390					395					400	
75	ctt	tta	acg	cta	atc	agc	cta	agc	gat	gac	gat	gat	tta	gac	ata	gat	1248
	Leu	Leu	Thr	Leu	Ile	Ser	Leu	Ser	Asp	Asp	Asp	Asp	Leu	Asp	Ile	Asp	
					405					410					415		
80	gaa	atc	aaa	gca	caa	att	att	gaa	ctg	caa	aaa	aag	caa	aat	cag	ctt	1296
	Glu	Ile	Lys	Ala	Gln	Ile	Ile	Glu	Leu	Gln	Lys	Lys	Gln	Asn	Gln	Leu	

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 5 act gaa aag tgt aac aga atc cag tca aaa atg aaa gtc cta gat gat 1344
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 435 440 445
 10 acg agc tca agt gaa aat gct cta aaa aga gcc atc gac tat ttt caa 1392
 Thr Ser Ser Ser Glu Asn Ala Leu Lys Arg Ala Ile Asp Tyr Phe Gln
 450 455 460
 15 tca atc ggt gca gat aac tta act ctt gaa gat aaa aaa aca att gtt 1440
 Ser Ile Gly Ala Asp Asn Leu Thr Leu Glu Asp Lys Lys Thr Ile Val
 465 470 475 480
 20 aac ttt atc gtg aaa gaa gtt acc att gtg gat tct gac acc ata tat 1488
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 40 Leu Glu Arg Pro Ala Leu Asn Arg Leu Arg Glu Asp Ala Ser Lys Gly
 50 55 60
 Leu Ile Ser Gln Val Ile Cys Tyr Asp Pro Asp Arg Leu Ser Arg Lys
 65 70 75 80
 45 Leu Met Asn Gln Leu Ile Ile Asp Asp Glu Leu Arg Lys Arg Asn Ile
 85 90 95
 Pro Leu Ile Phe Val Asn Gly Glu Tyr Ala Asn Ser Pro Glu Gly Gln
 100 105 110
 50 Leu Phe Phe Ala Met Arg Gly Ala Ile Ser Glu Phe Glu Lys Ala Lys
 115 120 125
 55 Ile Lys Glu Arg Thr Ser Ser Gly Arg Leu Gln Lys Met Lys Lys Gly
 130 135 140
 Met Ile Ile Lys Asp Ser Lys Leu Tyr Gly Tyr Lys Phe Val Lys Glu
 145 150 155 160
 60 Lys Arg Thr Leu Glu Ile Leu Glu Glu Glu Ala Lys Ile Ile Arg Met
 165 170 175
 Ile Phe Asn Tyr Phe Thr Asp His Lys Ser Pro Phe Phe Gly Arg Val
 180 185 190
 65 Asn Gly Ile Ala Leu His Leu Thr Gln Met Gly Val Lys Thr Lys Lys
 195 200 205

Gly Ala Lys Val Trp His Arg Gln Val Val Arg Gln Ile Leu Met Asn
 210 215 220
 5 Ser Ser Tyr Lys Gly Glu His Arg Gln Tyr Lys Tyr Asp Thr Glu Gly
 225 230 235 240
 Ser Tyr Val Ser Lys Gln Ala Gly Asn Lys Ser Ile Ile Lys Ile Arg
 245 250 255
 10 Pro Glu Glu Glu Gln Ile Thr Val Thr Ile Pro Ala Ile Val Pro Ala
 260 265 270
 15 Glu Gln Trp Asp Tyr Ala Gln Glu Leu Leu Gly Gln Ser Lys Arg Lys
 275 280 285
 His Leu Ser Ile Ser Pro His Asn Tyr Leu Leu Ser Gly Leu Val Arg
 290 295 300
 20 Cys Gly Lys Cys Gly Asn Thr Met Thr Gly Lys Lys Arg Lys Ser His
 305 310 315 320
 Gly Lys Asp Tyr Tyr Val Tyr Thr Cys Arg Lys Asn Tyr Ser Gly Ala
 325 330 335
 25 Lys Asp Arg Gly Cys Gly Lys Glu Met Ser Glu Asn Lys Leu Asn Arg
 340 345 350
 30 His Val Trp Gly Glu Ile Phe Lys Phe Ile Thr Asn Pro Gln Lys Tyr
 355 360 365
 Val Ser Phe Lys Glu Ala Glu Gln Ser Asn His Leu Ser Asp Glu Leu
 370 375 380
 35 Glu Leu Ile Glu Lys Glu Ile Glu Lys Thr Lys Lys Gly Arg Lys Arg
 385 390 395 400
 Leu Leu Thr Leu Ile Ser Leu Ser Asp Asp Asp Leu Asp Ile Asp
 405 410 415
 40 Glu Ile Lys Ala Gln Ile Ile Glu Leu Gln Lys Lys Gln Asn Gln Leu
 420 425 430
 45 Thr Glu Lys Cys Asn Arg Ile Gln Ser Lys Met Lys Val Leu Asp Asp
 435 440 445
 Thr Ser Ser Ser Glu Asn Ala Leu Lys Arg Ala Ile Asp Tyr Phe Gln
 450 455 460
 50 Ser Ile Gly Ala Asp Asn Leu Thr Leu Glu Asp Lys Lys Thr Ile Val
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	Asp Lys Gly Ala Leu Arg Lys Gln Ile Glu Arg Leu Arg Asn Ala Gly	
	20 25 30	
15	tgt tca aaa gtg tac tgg gat att caa tcg cgg aca.act gaa gtc aga	144
	Cys Ser Lys Val Tyr Trp Asp Ile Gln Ser Arg Thr Thr Glu Val Arg	
	35 40 45	
20	gaa ggg cta caa caa tta att aat gac tta aag aca tct tca aca ggt	192
	Glu Gly Leu Gln Gln Leu Ile Asn Asp Leu Lys Thr Ser Ser Thr Gly	
	50 55 60	
25	aag gta aaa tca ctg caa ttt acc cgc att gat cgc atc ggc tca tca	240
	Lys Val Lys Ser Leu Gln Phe Thr Arg Ile Asp Arg Ile Gly Ser Ser	
	65 70 75 80	
30	tcg cgg ttg ttt tat tca ttg tta gag gta tta cgt tcc aag gga att	288
	Ser Arg Leu Phe Tyr Ser Leu Leu Glu Val Leu Arg Ser Lys Gly Ile	
	85 90 95	
35	aaa ctg ata gcc tta gat caa ggc gtt gac cca gac agc ctt ggc ggg	336
	Lys Leu Ile Ala Leu Asp Gln Gly Val Asp Pro Asp Ser Leu Gly Gly	
	100 105 110	
40	gaa cta aca att gat atg tta ctg gct gct gcc aaa ttt gag gta aga	384
	Glu Leu Thr Ile Asp Met Leu Leu Ala Ala Lys Phe Glu Val Arg	
	115 120 125	
45	atg gtg acg gag agg tta aaa agc gaa cgt cgt cat agg gtg aac caa	432
	Met Val Thr Glu Arg Leu Lys Ser Glu Arg Arg His Arg Val Asn Gln	
	130 135 140	
50	gga aaa agt cac cga gtt gcc cca tta gga tac cgc aaa gat aaa gat	480
	Gly Lys Ser His Arg Val Ala Pro Leu Gly Tyr Arg Lys Asp Lys Asp	
	145 150 155 160	
55	aaa tat ata cgc gat cgc tca cca tgt gtt tgc tta cta gaa gga cgc	528
	Lys Tyr Ile Arg Asp Arg Ser Pro Cys Val Cys Leu Leu Glu Gly Arg	
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60	aga gaa tta acg gtg tct gac tta gcc cag tat att ttt cac act ttt	576
	Arg Glu Leu Thr Val Ser Asp Leu Ala Gln Tyr Ile Phe His Thr Phe	
	180 185 190	
65	ttt gag tgc ggt tcc gtt gct gct act gtg cgt aag ctg cac tca gat	624
	Phe Glu Cys Gly Ser Val Ala Ala Thr Val Arg Lys Leu His Ser Asp	
	195 200 205	
70	ttt ggt ata gaa aca aaa gtt ctg aat tgg aac aag cta gaa aaa tct	672
	Phe Gly Ile Glu Thr Lys Val Leu Asn Trp Asn Lys Leu Glu Lys Ser	
	210 215 220	
75	tcc cgg att gtt ggc gac gac gac tta gat aaa att gca ttt aca cca	720
	Ser Arg Ile Val Gly Asp Asp Asp Leu Asp Lys Ile Ala Phe Thr Pro	
	225 230 235 240	
80	aat aaa act aac cac ccc ttg cgt tat ccc tgg tct ggg cta aga tgg	768
	Asn Lys Thr Asn His Pro Leu Arg Tyr Pro Trp Ser Gly Leu Arg Trp	
	245 250 255	

	tca atc cct ggt tta aaa gcg tta tta gtt aac cct gtt tac gcc ggg	816
	Ser Ile Pro Gly Leu Lys Ala Leu Leu Val Asn Pro Val Tyr Ala Gly	
	260 265 270	
5	ggt ttg ccc ttt gat act tac gtt aaa tca aaa gga aaa cgc aag cat	864
	Gly Leu Pro Phe Asp Thr Tyr Val Lys Ser Lys Gly Lys Arg Lys His	
	275 280 285	
10	ttt gac gag tgg aaa gta aaa tgg gga acc cac gac gat gag gca atc	912
	Phe Asp Glu Trp Lys Val Lys Trp Gly Thr His Asp Asp Glu Ala Ile	
	290 295 300	
15	att acc tgt gag gaa cat gaa aga ata aaa cag atg att cga gac aat	960
	Ile Thr Cys Glu Glu His Glu Arg Ile Lys Gln Met Ile Arg Asp Asn	
	305 310 315 320	
	cgc aat aat cga tgg gct gca aga gaa gaa aac gaa gta aac cca ttt	1008
	Arg Asn Asn Arg Trp Ala Ala Arg Glu Glu Asn Glu Val Asn Pro Phe	
	325 330 335	
0	tct aat tta ctt aaa tgt acc cat tgc ggc ggc tca atg aca cgc cac	1056
	Ser Asn Leu Leu Lys Cys Thr His Cys Gly Gly Ser Met Thr Arg His	
	340 345 350	
5	gcc aaa cgt gta gat aag agt gga caa gct atc tat tat tat cag tgc	1104
	Ala Lys Arg Val Asp Lys Ser Gly Gln Ala Ile Tyr Tyr Tyr Gln Cys	
	355 360 365	
0	cga ttg tat aaa gct ggc aac tgt agc aat aaa aat atg att tca tcc	1152
	Arg Leu Tyr Lys Ala Gly Asn Cys Ser Asn Lys Asn Met Ile Ser Ser	
	370 375 380	
5	aaa ata tta gat atc caa gta atg gat tta ttg gca caa gaa gcc gaa	1200
	Lys Ile Leu Asp Ile Gln Val Met Asp Leu Leu Ala Gln Glu Ala Glu	
	385 390 395 400	
40	cgt tta gca aat ttg gtg gaa aca gat gag ccg ctt att gta gaa gaa	1248
	Arg Leu Ala Asn Leu Val Glu Thr Asp Glu Pro Leu Ile Val Glu Glu	
	405 410 415	
	ccc cca gaa gta aaa acg ctg cgc gca tcc ctg aat agt ctg gaa aca	1296
	Pro Pro Glu Val Lys Thr Leu Arg Ala Ser Leu Asn Ser Leu Glu Thr	
	420 425 430	
45	ttg cca gca agt tca gca att gaa caa att aaa aat gac ctc aaa gaa	1344
	Leu Pro Ala Ser Ser Ala Ile Glu Gln Ile Lys Asn Asp Leu Lys Glu	
	435 440 445	
50	cag att gcg atc gca cta gga gca acc aat aat gct tct aaa caa tct	1392
	Gln Ile Ala Ile Ala Leu Gly Ala Thr Asn Asn Ala Ser Lys Gln Ser	
	450 455 460	
55	ctg att gcc aag gaa aga att ata caa gct ttt gct cat aaa agt tac	1440
	Leu Ile Ala Lys Glu Arg Ile Ile Gln Ala Phe Ala His Lys Ser Tyr	
	465 470 475 480	
60	tgg caa gga cta aac gct caa gat aaa cga gca atc ctc aat ggt tgc	1488
	Trp Gln Gly Leu Asn Ala Gln Asp Lys Arg Ala Ile Leu Asn Gly Cys	
	485 490 495	
65	gta aaa aaa atc tcc gta gat ggt aac ttt gtt aca gct att gag tat	1536
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 35 40 45

Glu Gly Leu Gln Gln Leu Ile Asn Asp Leu Lys Thr Ser Ser Thr Gly
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20 Lys Val Lys Ser Leu Gln Phe Thr Arg Ile Asp Arg Ile Gly Ser Ser
 65 70 75 80

Ser Arg Leu Phe Tyr Ser Leu Leu Glu Val Leu Arg Ser Lys Gly Ile
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25 Lys Leu Ile Ala Leu Asp Gln Gly Val Asp Pro Asp Ser Leu Gly Gly
 100 105 110

30 Glu Leu Thr Ile Asp Met Leu Leu Ala Ala Ala Lys Phe Glu Val Arg
 115 120 125

Met Val Thr Glu Arg Leu Lys Ser Glu Arg Arg His Arg Val Asn Gln
 130 135 140

35 Gly Lys Ser His Arg Val Ala Pro Leu Gly Tyr Arg Lys Asp Lys Asp
 145 150 155 160

40 Lys Tyr Ile Arg Asp Arg Ser Pro Cys Val Cys Leu Leu Glu Gly Arg
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Arg Glu Leu Thr Val Ser Asp Leu Ala Gln Tyr Ile Phe His Thr Phe
 180 185 190

45 Phe Glu Cys Gly Ser Val Ala Ala Thr Val Arg Lys Leu His Ser Asp
 195 200 205

Phe Gly Ile Glu Thr Lys Val Leu Asn Trp Asn Lys Leu Glu Lys Ser
 210 215 220

50 Ser Arg Ile Val Gly Asp Asp Asp Leu Asp Lys Ile Ala Phe Thr Pro
 225 230 235 240

Asn Lys Thr Asn His Pro Leu Arg Tyr Pro Trp Ser Gly Leu Arg Trp
 245 250 255

55 Ser Ile Pro Gly Leu Lys Ala Leu Leu Val Asn Pro Val Tyr Ala Gly
 260 265 270

60 Gly Leu Pro Phe Asp Thr Tyr Val Lys Ser Lys Gly Lys Arg Lys His
 275 280 285

Phe Asp Glu Trp Lys Val Lys Trp Gly Thr His Asp Asp Glu Ala Ile
 290 295 300

65 Ile Thr Cys Glu Glu His Glu Arg Ile Lys Gln Met Ile Arg Asp Asn
 305 310 315 320

Arg Asn Asn Arg Trp Ala Ala Arg Glu Glu Asn Glu Val Asn Pro Phe
 325 330 335
 5 Ser Asn Leu Leu Lys Cys Thr His Cys Gly Gly Ser Met Thr Arg His
 340 345 350
 Ala Lys Arg Val Asp Lys Ser Gly Gln Ala Ile Tyr Tyr Tyr Gln Cys
 355 360 365
 10 Arg Leu Tyr Lys Ala Gly Asn Cys Ser Asn Lys Asn Met Ile Ser Ser
 370 375 380
 Lys Ile Leu Asp Ile Gln Val Met Asp Leu Leu Ala Gln Glu Ala Glu
 385 390 395 400
 15 Arg Leu Ala Asn Leu Val Glu Thr Asp Glu Pro Leu Ile Val Glu Glu
 405 410 415
 0 Pro Pro Glu Val Lys Thr Leu Arg Ala Ser Leu Asn Ser Leu Glu Thr
 420 425 430
 Leu Pro Ala Ser Ser Ala Ile Glu Gln Ile Lys Asn Asp Leu Lys Glu
 435 440 445
 25 Gln Ile Ala Ile Ala Leu Gly Ala Thr Asn Asn Ala Ser Lys Gln Ser
 450 455 460
 Leu Ile Ala Lys Glu Arg Ile Ile Gln Ala Phe Ala His Lys Ser Tyr
 465 470 475 480
 30 Trp Gln Gly Leu Asn Ala Gln Asp Lys Arg Ala Ile Leu Asn Gly Cys
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 Asp Asp Asp Leu Thr Gly Glu Ser Asn Ser Ile Thr Asn Gln Lys Lys
 20 25 30
 60 tac ctc gaa gat tat gcc cgt agg aat ggt ttt gag aac att cgc cat 144
 Tyr Leu Glu Asp Tyr Ala Arg Arg Asn Gly Phe Glu Asn Ile Arg His
 35 40 45
 65 ttt acc gat gac gga ttt tcg ggt gta aat ttc aat cgc cct ggc ttt 192
 Phe Thr Asp Asp Gly Phe Ser Gly Val Asn Phe Asn Arg Pro Gly Phe
 50 55 60

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	65 70 75 80	
5	gtt aag gat atg agc cga ttg ggg cga aat tat ctg caa gta ggt ttt	288
	Val Lys Asp Met Ser Arg Leu Gly Arg Asn Tyr Leu Gln Val Gly Phe	
	85 90 95	
10	tat acg gaa gtt ctg ttt cca cag aaa aat gtc cgt ttc ctt gca att	336
	Tyr Thr Glu Val Leu Phe Pro Gln Lys Asn Val Arg Phe Leu Ala Ile	
	100 105 110	
15	aac aac agt att gac agt aac aac gct tgc gat aat gac ttt gct ccg	384
	Asn Asn Ser Ile Asp Ser Asn Asn Ala Ser Asp Asn Asp Phe Ala Pro	
	115 120 125	
20	ttt ttg aat att atg aac gaa tgg tat gcc aaa gac aca agc aac aaa	432
	Phe Leu Asn Ile Met Asn Glu Trp Tyr Ala Lys Asp Thr Ser Asn Lys	
	130 135 140	
25	atc aag gct ata ttc gat gcc cgt atg aaa gac gga aag cgt tgt agc	480
	Ile Lys Ala Ile Phe Asp Ala Arg Met Lys Asp Gly Lys Arg Cys Ser	
	145 150 155 160	
30	ggg tct atc cct tat ggg tat aac cga ctg ccg agc gac aaa caa acg	528
	Gly Ser Ile Pro Tyr Gly Tyr Asn Arg Leu Pro Ser Asp Lys Gln Thr	
	165 170 175	
35	ctt gtg gtt gac cct gtg gct tgc gaa gtg gta aag cgt atc ttt act	576
	Leu Val Val Asp Pro Val Ala Ser Glu Val Val Lys Arg Ile Phe Thr	
	180 185 190	
40	ctt gcc aat gat ggc aaa agt aca agg gca atc gca gaa ata ctg acc	624
	Leu Ala Asn Asp Gly Lys Ser Thr Arg Ala Ile Ala Glu Ile Leu Thr	
	195 200 205	
45	gaa gaa aaa gtt tta acc cct gcg gca tac gca aag gaa tac cac ccc	672
	Glu Glu Lys Val Leu Thr Pro Ala Ala Tyr Ala Lys Glu Tyr His Pro	
	210 215 220	
50	gaa cag tac aac ggc aac aag ttc aca aac cct tat ctt tgg gca atg	720
	Glu Gln Tyr Asn Gly Asn Lys Phe Thr Asn Pro Tyr Leu Trp Ala Met	
	225 230 235 240	
55	tca acg ata aga aat att tta ggc agg cag gaa tat ctc ggt cac acc	768
	Ser Thr Ile Arg Asn Ile Leu Gly Arg Gln Glu Tyr Leu Gly His Thr	
	245 250 255	
60	gtt ttg cga aag tgc gta agc aca aat ttc aaa ctt cac aag aga aaa	816
	Val Leu Arg Lys Ser Val Ser Thr Asn Phe Lys Leu His Lys Arg Lys	
	260 265 270	
65	agc aca gac gaa gaa gaa cag tat gta ttt ccg aat aca cac gag cct	864
	Ser Thr Asp Glu Glu Glu Gln Tyr Val Phe Pro Asn Thr His Glu Pro	
	275 280 285	
70	atc ata tgc cag gaa ctt tgg gac agc gtt caa aaa cgc aga agc aga	912
	Ile Ile Ser Gln Glu Leu Trp Asp Ser Val Gln Lys Arg Arg Ser Arg	
	290 295 300	
75	gta aat cgt gcc tgc gct tgg gga acg cac agc aac cgt tta agc gga	960
	Val Asn Arg Ala Ser Ala Trp Gly Thr His Ser Asn Arg Leu Ser Gly	
	305 310 315 320	
80	tat ttg tac tgt gcc gat tgc gga aga aga atg act ttg cag aca cat	1008
	Tyr Leu Tyr Cys Ala Asp Cys Gly Arg Arg Met Thr Leu Gln Thr His	
	325 330 335	

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10	tat gca agc aga gtg aac agt tgt acc agt cat tcg att agt acc gat Tyr Ala Ser Arg Val Asn Ser Cys Thr Ser His Ser Ile Ser Thr Asp 355 360 365	1104
15	aat gtt gaa gcc ttg ata tta tca tct gtc aaa cgc ttt tca agg ttt Asn Val Glu Ala Leu Ile Leu Ser Ser Val Lys Arg Phe Ser Arg Phe 370 375 380	1152
20	gtt ctg aat gat gaa caa gca ttt gct ttg gaa ctg caa tct ctt tgg Val Leu Asn Asp Glu Gln Ala Phe Ala Leu Glu Leu Gln Ser Leu Trp 385 390 395 400	1200
25	aat gaa aaa cag gag gaa aag ccg aaa cac aat caa tcg gaa ctg caa Asn Glu Lys Gln Glu Glu Lys Pro Lys His Asn Gln Ser Glu Leu Gln 405 410 415	1248
30	cgc tgt cag aaa cgc tat gac gaa ctc tct acc ctt gtt cgt ggc ttg Arg Cys Gln Lys Arg Tyr Asp Glu Leu Ser Thr Leu Val Arg Gly Leu 420 425 430	1296
35	tat gaa aat ctt atg tcg gga tta ctg ccc gaa aga cag tat aag caa Tyr Glu Asn Leu Met Ser Gly Leu Leu Pro Glu Arg Gln Tyr Lys Gln 435 440 445	1344
40	ctg atg aaa cag tat gat gac gag cag gca gag ttg gaa acg aaa atg Leu Met Lys Gln Tyr Asp Asp Glu Gln Ala Glu Leu Glu Thr Lys Met 450 455 460	1392
45	gaa acg atg aaa aca gaa ctt gcc gaa gaa aaa gta agt tcc gtt gat Glu Thr Met Lys Thr Glu Leu Ala Glu Glu Lys Val Ser Ser Val Asp 465 470 475 480	1440
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55	atc tcc gat aca atg ttt aat gaa ctt gtt gat aag ata gtg gtt tat Ile Ser Asp Thr Met Phe Asn Glu Leu Val Asp Lys Ile Val Val Tyr 500 505 510	1536
60	gaa gca gag ggt gtg gga aaa gca cga aca caa aag gtc gat att tat Glu Ala Glu Gly Val Gly Lys Ala Arg Thr Gln Lys Val Asp Ile Tyr 515 520 525	1584
65	ttt aac tat gtc ggt caa gtg gat att gcc tat acc gaa gaa gaa ctt Phe Asn Tyr Val Gly Gln Val Asp Ile Ala Tyr Thr Glu Glu Glu Leu 530 535 540	1632
70	gcc gag ata gaa aca cag aaa gag cag gag gaa cag caa cgc ttg gca Ala Glu Ile Glu Thr Gln Lys Glu Gln Glu Glu Gln Gln Arg Leu Ala 545 550 555 560	1680
75	aga cag cgc aag cgt gaa aaa gcc tac cga gaa aag cga aag gca cag Arg Gln Arg Lys Arg Glu Lys Ala Tyr Arg Glu Lys Arg Lys Ala Gln 565 570 575	1728
80	aaa atc gct gaa aac ggt ggc gaa atc gtt aag aca aag gtt tgc cct Lys Ile Ala Glu Asn Gly Gly Glu Ile Val Lys Thr Lys Val Cys Pro 580 585 590	1776
85	cat tgc aac aaa gag ttt atc ccg aca agc aac cga cag gtg ttc tgt His Cys Asn Lys Glu Phe Ile Pro Thr Ser Asn Arg Gln Val Phe Cys 600 605 610	1824

595 600 605

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 625 630 635 640

15 gtg tgc ggc aat tcc tat tgg cct aca cac agc caa cag aaa ttc tgc 1968
 Val Cys Gly Asn Ser Tyr Trp Pro Thr His Ser Gln Gln Lys Phe Cys
 645 650 655

20 tcc gaa gaa tgt caa agg gta aat cac aat aag aaa aca ttg gaa ttt 2016
 Ser Glu Glu Cys Gln Arg Val Asn His Asn Lys Lys Thr Leu Glu Phe
 660 665 670

25 tac cac cat aaa aaa gaa aag gag aag ctg caa tgc aaa gat tta tca 2064
 Tyr His His Lys Lys Glu Lys Glu Lys Leu Gln Cys Lys Asp Leu Ser
 675 680 685

30 cag acg aaa gaa cgg gta tcc gat atg aac tta tcg ggg act att act 2112
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35 acc cct gct taa 2124
 Thr Pro Ala
 705

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 <212> PRT
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55 Tyr Leu Glu Asp Tyr Ala Arg Arg Asn Gly Phe Glu Asn Ile Arg His
 35 40 45

60 Phe Thr Asp Asp Gly Phe Ser Gly Val Asn Phe Asn Arg Pro Gly Phe
 50 55 60

65 Gln Ser Leu Ile Lys Glu Val Glu Ala Gly Asn Val Glu Thr Leu Ile
 65 70 75 80

70 Val Lys Asp Met Ser Arg Leu Gly Arg Asn Tyr Leu Gln Val Gly Phe
 85 90 95

75 Tyr Thr Glu Val Leu Phe Pro Gln Lys Asn Val Arg Phe Leu Ala Ile
 100 105 110

80 Asn Asn Ser Ile Asp Ser Asn Asn Ala Ser Asp Asn Asp Phe Ala Pro
 115 120 125

85 Phe Leu Asn Ile Met Asn Glu Trp Tyr Ala Lys Asp Thr Ser Asn Lys
 130 135 140

90 Ile Lys Ala Ile Phe Asp Ala Arg Met Lys Asp Gly Lys Arg Cys Ser
 145 150 155 160

Gly Ser Ile Pro Tyr Gly Tyr Asn Arg Leu Pro Ser Asp Lys Gln Thr
 165 170 175
 5 Leu Val Val Asp Pro Val Ala Ser Glu Val Val Lys Arg Ile Phe Thr
 180 185 190
 Leu Ala Asn Asp Gly Lys Ser Thr Arg Ala Ile Ala Glu Ile Leu Thr
 195 200 205
 10 Glu Glu Lys Val Leu Thr Pro Ala Ala Tyr Ala Lys Glu Tyr His Pro
 210 215 220
 Glu Gln Tyr Asn Gly Asn Lys Phe Thr Asn Pro Tyr Leu Trp Ala Met
 225 230 235 240
 15 Ser Thr Ile Arg Asn Ile Leu Gly Arg Gln Glu Tyr Leu Gly His Thr
 245 250 255
 Val Leu Arg Lys Ser Val Ser Thr Asn Phe Lys Leu His Lys Arg Lys
 260 265 270
 Ser Thr Asp Glu Glu Glu Gln Tyr Val Phe Pro Asn Thr His Glu Pro
 275 280 285
 25 Ile Ile Ser Gln Glu Leu Trp Asp Ser Val Gln Lys Arg Arg Ser Arg
 290 295 300
 Val Asn Arg Ala Ser Ala Trp Gly Thr His Ser Asn Arg Leu Ser Gly
 305 310 315 320
 30 Tyr Leu Tyr Cys Ala Asp Cys Gly Arg Arg Met Thr Leu Gln Thr His
 325 330 335
 Tyr Ser Lys Lys Asp Gly Ser Val Gln Tyr Ser Tyr Arg Cys Gly Gly
 340 345 350
 35 Tyr Ala Ser Arg Val Asn Ser Cys Thr Ser His Ser Ile Ser Thr Asp
 355 360 365
 40 Asn Val Glu Ala Leu Ile Leu Ser Ser Val Lys Arg Phe Ser Arg Phe
 370 375 380
 Val Leu Asn Asp Glu Gln Ala Phe Ala Leu Glu Leu Gln Ser Leu Trp
 385 390 395 400
 45 Asn Glu Lys Gln Glu Glu Lys Pro Lys His Asn Gln Ser Glu Leu Gln
 405 410 415
 Arg Cys Gln Lys Arg Tyr Asp Glu Leu Ser Thr Leu Val Arg Gly Leu
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 Tyr Glu Asn Leu Met Ser Gly Leu Leu Pro Glu Arg Gln Tyr Lys Gln
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 Glu Thr Met Lys Thr Glu Leu Ala Glu Glu Lys Val Ser Ser Val Asp
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 60 Ile Lys His Phe Ile Ser Leu Ile Arg Lys Cys Lys Asn Pro Thr Glu
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 Ile Ser Asp Thr Met Phe Asn Glu Leu Val Asp Lys Ile Val Val Tyr
 500 505 510
 Glu Ala Glu Gly Val Gly Lys Ala Arg Thr Gln Lys Val Asp Ile Tyr

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	530		535		540	
5	Ala Glu Ile Glu Thr Gln Lys Glu Gln Glu Glu Gln Gln Arg Leu Ala					
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		565		570		575
	Lys Ile Ala Glu Asn Gly Gly Glu Ile Val Lys Thr Lys Val Cys Pro					
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15	His Cys Asn Lys Glu Phe Ile Pro Thr Ser Asn Arg Gln Val Phe Cys					
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	Ser Lys Glu Cys Cys Tyr Gln Ala Arg Gln Asp Lys Lys Lys Thr Asp					
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20	Arg Glu Ala Glu Arg Gly Asn His Tyr Tyr Arg Gln Arg Val Cys Ala					
	625		630		635	640
	Val Cys Gly Asn Ser Tyr Trp Pro Thr His Ser Gln Gln Lys Phe Cys					
25		645		650		655
	Ser Glu Glu Cys Gln Arg Val Asn His Asn Lys Lys Thr Leu Glu Phe					
		660		665		670
30	Tyr His His Lys Lys Glu Lys Glu Lys Leu Gln Cys Lys Asp Leu Ser					
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55	gag cca ctt tca tct acc gac ggc agt ttt ctc ggc tca agt ctg caa					96
	Glu Pro Leu Ser Ser Thr Asp Gly Ser Phe Leu Gly Ser Ser Leu Gln					
		20		25		30
60	gca cag cag caa aga gaa cac atg aga aca aaa gta cta caa gac cta					144
	Ala Gln Gln Gln Arg Glu His Met Arg Thr Lys Val Leu Gln Asp Leu					
		35		40		45
	gac aag gta aat ctg cgt ttg aag tct gca aag acg aaa gtc tca gtt					192
	Asp Lys Val Asn Leu Arg Leu Lys Ser Ala Lys Thr Lys Val Ser Val					
65		50		55		60
	cga gaa tct aac gga agt ctg caa tta cga gca acg tta cca att aaa					240

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5	cct	gga	gat	aag	gac	acc	aac	ggt	aca	ggc	aga	aag	caa	tac	aat	ctc	288
	Pro	Gly	Asp	Lys	Asp	Thr	Asn	Gly	Thr	Gly	Arg	Lys	Gln	Tyr	Asn	Leu	
					85					90					95		
10	agc	ttg	aat	atc	cct	gca	aac	ttg	gat	gga	ctg	aag	acg	gct	gag	gaa	336
	Ser	Leu	Asn	Ile	Pro	Ala	Asn	Leu	Asp	Gly	Leu	Lys	Thr	Ala	Glu	Glu	
				100					105					110			
15	gaa	gct	tat	gaa	tta	ggt	aaa	tta	atc	gct	cgg	aaa	acc	ttt	gaa	tggt	384
	Glu	Ala	Tyr	Glu	Leu	Gly	Lys	Leu	Ile	Ala	Arg	Lys	Thr	Phe	Glu	Trp	
			115					120					125				
20	aat	gat	aaa	tat	tta	ggc	aaa	gaa	gcc	act	aaa	aaa	gat	tca	caa	aca	432
	Asn	Asp	Lys	Tyr	Leu	Gly	Lys	Glu	Ala	Thr	Lys	Lys	Asp	Ser	Gln	Thr	
		130					135					140					
25	ata	ggt	gat	tta	cta	gaa	aaa	ttt	gca	gaa	gag	tat	ttt	aaa	acc	cat	480
	Ile	Gly	Asp	Leu	Leu	Glu	Lys	Phe	Ala	Glu	Glu	Tyr	Phe	Lys	Thr	His	
		145				150					155				160		
30	aaa	cgc	acc	act	aaa	agc	gaa	cat	acc	ttt	ttt	tac	tat	ttt	tcc	cgc	528
	Lys	Arg	Thr	Thr	Lys	Ser	Glu	His	Thr	Phe	Phe	Tyr	Tyr	Phe	Ser	Arg	
					165				170						175		
35	acc	caa	cga	tat	acc	aat	tcc	aaa	gat	tta	gca	acg	gcg	gaa	aat	ctc	576
	Thr	Gln	Arg	Tyr	Thr	Asn	Ser	Lys	Asp	Leu	Ala	Thr	Ala	Glu	Asn	Leu	
				180					185					190			
40	atc	aat	tca	att	gag	caa	atc	gat	aaa	gaa	tggt	gcg	aga	tat	aat	gcc	624
	Ile	Asn	Ser	Ile	Glu	Gln	Ile	Asp	Lys	Glu	Trp	Ala	Arg	Tyr	Asn	Ala	
			195					200					205				
45	gcc	aga	gcc	ata	tca	gct	ttt	tgc	ata	aca	ttc	aat	ata	gaa	att	gat	672
	Ala	Arg	Ala	Ile	Ser	Ala	Phe	Cys	Ile	Thr	Phe	Asn	Ile	Glu	Ile	Asp	
		210					215					220					
50	ttg	tcc	cag	tat	tcc	aaa	atg	cct	gat	cgc	aat	tcg	cgc	aac	atc	ccc	720
	Leu	Ser	Gln	Tyr	Ser	Lys	Met	Pro	Asp	Arg	Asn	Ser	Arg	Asn	Ile	Pro	
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55	aca	gat	gca	gaa	ata	cta	tca	gga	att	acc	aaa	ttt	gaa	gac	tat	cta	768
	Thr	Asp	Ala	Glu	Ile	Leu	Ser	Gly	Ile	Thr	Lys	Phe	Glu	Asp	Tyr	Leu	
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60	gtt	acc	aga	gga	aat	caa	gtt	aat	gaa	gat	gta	aaa	gat	agc	tggt	caa	816
	Val	Thr	Arg	Gly	Asn	Gln	Val	Asn	Glu	Asp	Val	Lys	Asp	Ser	Trp	Gln	
				260					265					270			
65	ctt	tggt	cgc	tggt	aca	tat	gga	atg	tta	gca	gtt	ttt	gggt	tta	cgc	ccc	864
	Leu	Trp	Arg	Trp	Thr	Tyr	Gly	Met	Leu	Ala	Val	Phe	Gly	Leu	Arg	Pro	
			275					280					285				
70	agg	gaa	att	ttt	att	aac	cct	aat	att	gat	tggt	tggt	tta	agc	aaa	gag	912
	Arg	Glu	Ile	Phe	Ile	Asn	Pro	Asn	Ile	Asp	Trp	Trp	Leu	Ser	Lys	Glu	
		290					295					300					
75	aat	ata	gac	ctc	aca	tggt	aaa	gta	gac	aaa	gaa	tgt	aaa	act	gggt	gaa	960
	Asn	Ile	Asp	Leu	Thr	Trp	Lys	Val	Asp	Lys	Glu	Cys	Lys	Thr	Gly	Glu	
						310					315					320	
80	aga	caa	gca	tta	ccc	tta	cat	aaa	gaa	tggt	att	gat	gag	ttt	gat	tta	1008
	Arg	Gln	Ala	Leu	Pro	Leu	His	Lys	Glu	Trp	Ile	Asp	Glu	Phe	Asp	Leu	
				325						330					335		

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 Arg Asn Pro Lys Tyr Leu Glu Met Leu Ala Thr Ala Ile Ser Lys Lys
 340 345 350

5 gat aaa aca aat cat gct gaa ata aca gcc tta act cag cgt att agt 1104
 Asp Lys Thr Asn His Ala Glu Ile Thr Ala Leu Thr Gln Arg Ile Ser
 355 360 365

10 tgg tgg ttt ccg aaa gtc gaa tta gat ttt aaa ccc tat gat tta cgt 1152
 Trp Trp Phe Arg Lys Val Glu Leu Asp Phe Lys Pro Tyr Asp Leu Arg
 370 375 380

15 cac gcc tgg gca atc aga gcg cat att tta ggc ata cca atc aaa gcg 1200
 His Ala Trp Ala Ile Arg Ala His Ile Leu Gly Ile Pro Ile Lys Ala
 385 390 395 400

20 gcg gct gat aat ttg ggg cat agt atg cag gtt cat aca caa acc tat 1248
 Ala Ala Asp Asn Leu Gly His Ser Met Gln Val His Thr Gln Thr Tyr
 405 410 415

cag cgc tgg ttc tcg cta gat atg cgg aag tta gcg att aat cag gct 1296
 Gln Arg Trp Phe Ser Leu Asp Met Arg Lys Leu Ala Ile Asn Gln Ala
 420 425 430

25 ttg act aag agg aat gaa ttt gag gtg att agg gag gag aat gct aaa 1344
 Leu Thr Lys Arg Asn Glu Phe Glu Val Ile Arg Glu Glu Asn Ala Lys
 435 440 445

30 ttg cag ata gaa aat gaa agg ttg agg atg gaa att gag aag tta aag 1392
 Leu Gln Ile Glu Asn Glu Arg Leu Arg Met Glu Ile Glu Lys Leu Lys
 450 455 460

35 atg gaa ata gct tat aag aat agt tgag 1420
 Met Glu Ile Ala Tyr Lys Asn Ser
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50 Ala Gln Gln Gln Arg Glu His Met Arg Thr Lys Val Leu Gln Asp Leu
 35 40 45

55 Asp Lys Val Asn Leu Arg Leu Lys Ser Ala Lys Thr Lys Val Ser Val
 50 55 60

Arg Glu Ser Asn Gly Ser Leu Gln Leu Arg Ala Thr Leu Pro Ile Lys
 65 70 75 80

60 Pro Gly Asp Lys Asp Thr Asn Gly Thr Gly Arg Lys Gln Tyr Asn Leu
 85 90 95

Ser Leu Asn Ile Pro Ala Asn Leu Asp Gly Leu Lys Thr Ala Glu Glu
 100 105 110

65 Glu Ala Tyr Glu Leu Gly Lys Leu Ile Ala Arg Lys Thr Phe Glu Trp
 115 120 125

Asn Asp Lys Tyr Leu Gly Lys Glu Ala Thr Lys Lys Asp Ser Gln Thr
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 5 Ile Gly Asp Leu Leu Glu Lys Phe Ala Glu Glu Tyr Phe Lys Thr His
 145 150 155 160
 Lys Arg Thr Thr Lys Ser Glu His Thr Phe Phe Tyr Tyr Phe Ser Arg
 165 170 175
 10 Thr Gln Arg Tyr Thr Asn Ser Lys Asp Leu Ala Thr Ala Glu Asn Leu
 180 185 190
 Ile Asn Ser Ile Glu Gln Ile Asp Lys Glu Trp Ala Arg Tyr Asn Ala
 195 200 205
 15 Ala Arg Ala Ile Ser Ala Phe Cys Ile Thr Phe Asn Ile Glu Ile Asp
 210 215 220
 20 Leu Ser Gln Tyr Ser Lys Met Pro Asp Arg Asn Ser Arg Asn Ile Pro
 225 230 235 240
 Thr Asp Ala Glu Ile Leu Ser Gly Ile Thr Lys Phe Glu Asp Tyr Leu
 245 250 255
 25 Val Thr Arg Gly Asn Gln Val Asn Glu Asp Val Lys Asp Ser Trp Gln
 260 265 270
 30 Leu Trp Arg Trp Thr Tyr Gly Met Leu Ala Val Phe Gly Leu Arg Pro
 275 280 285
 Arg Glu Ile Phe Ile Asn Pro Asn Ile Asp Trp Trp Leu Ser Lys Glu
 290 295 300
 35 Asn Ile Asp Leu Thr Trp Lys Val Asp Lys Glu Cys Lys Thr Gly Glu
 305 310 315 320
 Arg Gln Ala Leu Pro Leu His Lys Glu Trp Ile Asp Glu Phe Asp Leu
 325 330 335
 40 Arg Asn Pro Lys Tyr Leu Glu Met Leu Ala Thr Ala Ile Ser Lys Lys
 340 345 350
 Asp Lys Thr Asn His Ala Glu Ile Thr Ala Leu Thr Gln Arg Ile Ser
 355 360 365
 45 Trp Trp Phe Arg Lys Val Glu Leu Asp Phe Lys Pro Tyr Asp Leu Arg
 370 375 380
 50 His Ala Trp Ala Ile Arg Ala His Ile Leu Gly Ile Pro Ile Lys Ala
 385 390 395 400
 Ala Ala Asp Asn Leu Gly His Ser Met Gln Val His Thr Gln Thr Tyr
 405 410 415
 55 Gln Arg Trp Phe Ser Leu Asp Met Arg Lys Leu Ala Ile Asn Gln Ala
 420 425 430
 60 Leu Thr Lys Arg Asn Glu Phe Glu Val Ile Arg Glu Glu Asn Ala Lys
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 Leu Gln Ile Glu Asn Glu Arg Leu Arg Met Glu Ile Glu Lys Leu Lys
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 65 Met Glu Ile Ala Tyr Lys Asn Ser
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 Glu Arg Lys Gly Arg Tyr Tyr Val Tyr Lys Leu Glu Tyr Glu Asn Gly
 20 25 30
 25 gag gta aaa gag cgt tac gtg ggt cct tta gct gac gtc gtt gaa tca 144
 Glu Val Lys Glu Arg Tyr Val Gly Pro Leu Ala Asp Val Val Glu Ser
 35 40 45
 30 tat cta aaa atg aaa tta ggg gtc gta ggg gat act ccc cta caa gcg 192
 Tyr Leu Lys Met Lys Leu Gly Val Val Gly Asp Thr Pro Leu Gln Ala
 50 55 60
 35 gat ccc ccc ggt ttc gag ccc ggg aca agc gga agc ggt ggt gga aaa 240
 Asp Pro Pro Gly Phe Glu Pro Gly Thr Ser Gly Ser Gly Gly Lys
 65 70 75 80
 40 gag gga act gaa cga cgt aaa ata gcg ttg gtt gcc aat ttg cgc caa 288
 Glu Gly Thr Glu Arg Arg Lys Ile Ala Leu Val Ala Asn Leu Arg Gln
 85 90 95
 45 tac gcg acg gac ggc aac ata aag gcg ttc tac aac tat ctc atg aac 336
 Tyr Ala Thr Asp Gly Asn Ile Lys Ala Phe Tyr Asn Tyr Leu Met Asn
 100 105 110
 50 gaa agg ggg ata agc gaa aaa act gca aag gac tac atc aat gct ata 384
 Glu Arg Gly Ile Ser Glu Lys Thr Ala Lys Asp Tyr Ile Asn Ala Ile
 115 120 125
 55 tca aag ccg tat aaa gag acg aga gac gca cag aag gct tac cga ctc 432
 Ser Lys Pro Tyr Lys Glu Thr Arg Asp Ala Gln Lys Ala Tyr Arg Leu
 130 135 140
 60 ttt gca cgt ttc tta gcg tca cgc aat atc ata cat gat gaa ttt gcg 480
 Phe Ala Arg Phe Leu Ala Ser Arg Asn Ile Ile His Asp Glu Phe Ala
 145 150 155 160
 55 gat aaa ata ttg aaa gcg gta aag gtg aag aag gcg aac gct gat atc 528
 Asp Lys Ile Leu Lys Ala Val Lys Val Lys Lys Ala Asn Ala Asp Ile
 165 170 175
 60 tac att cca acg ttg gaa gag ata aaa agg acg tta caa tta gca aaa 576
 Tyr Ile Pro Thr Leu Glu Glu Ile Lys Arg Thr Leu Gln Leu Ala Lys
 180 185 190
 65 gac tat agc gaa aac gtc tac ttc atc tac cgt atc gct ctc gag tcg 624
 Asp Tyr Ser Glu Asn Val Tyr Phe Ile Tyr Arg Ile Ala Leu Glu Ser
 195 200 205

ggc gtt agg ctg agc gaa ata ctg aaa gtg ctg aag gaa ccc gaa agg 672
 Gly Val Arg Leu Ser Glu Ile Leu Lys Val Leu Lys Glu Pro Glu Arg
 210 215 220

5 gac att tgc ggt aac gac gtc tgt tat tat ccg ctt agt tgg act agg 720
 Asp Ile Cys Gly Asn Asp Val Cys Tyr Tyr Pro Leu Ser Trp Thr Arg
 225 230 235 240

10 gga tat aag ggc gtc ttc tat gta ttc cac ata acg cct ctg aag aga 768
 Gly Tyr Lys Gly Val Phe Tyr Val Phe His Ile Thr Pro Leu Lys Arg
 245 250 255

15 gta gag gtg acg aag tgg gca ata gcg gac ttt gaa cga cgt cat aag 816
 Val Glu Val Thr Lys Trp Ala Ile Ala Asp Phe Glu Arg Arg His Lys
 260 265 270

20 gac gct ata gcg ata aag tac ttc cgc aaa ttc gta gcg tct aag atg 864
 Asp Ala Ile Ala Ile Lys Tyr Phe Arg Lys Phe Val Ala Ser Lys Met
 275 280 285

25 gct gag cta agc gta ccg tta gat att atc gat ttt att caa ggg cgt 912
 Ala Glu Leu Ser Val Pro Leu Asp Ile Ile Asp Phe Ile Gln Gly Arg
 290 295 300

30 aaa ccg aca cgc gtt tta acg caa cat tac gta tcg ctc ttc ggc ata 960
 Lys Pro Thr Arg Val Leu Thr Gln His Tyr Val Ser Leu Phe Gly Ile
 305 310 315 320

35 gcg aaa gag caa tat aaa aag tat gcg gaa tgg cta aaa ggg gtc tga 1008
 Ala Lys Glu Gln Tyr Lys Lys Tyr Ala Glu Trp Leu Lys Gly Val
 325 330 335

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 <212> PRT
 <213> Artificial Sequence
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 20 25 30

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 35 40 45

Tyr Leu Lys Met Lys Leu Gly Val Val Gly Asp Thr Pro Leu Gln Ala
 50 55 60

55 Asp Pro Pro Gly Phe Glu Pro Gly Thr Ser Gly Ser Gly Gly Gly Lys
 65 70 75 80

Glu Gly Thr Glu Arg Arg Lys Ile Ala Leu Val Ala Asn Leu Arg Gln
 85 90 95

60 Tyr Ala Thr Asp Gly Asn Ile Lys Ala Phe Tyr Asn Tyr Leu Met Asn
 100 105 110

Glu Arg Gly Ile Ser Glu Lys Thr Ala Lys Asp Tyr Ile Asn Ala Ile
 115 120 125

65 Ser Lys Pro Tyr Lys Glu Thr Arg Asp Ala Gln Lys Ala Tyr Arg Leu
 130 135 140

Phe Ala Arg Phe Leu Ala Ser Arg Asn Ile Ile His Asp Glu Phe Ala
 145 150 155 160
 5 Asp Lys Ile Leu Lys Ala Val Lys Val Lys Lys Ala Asn Ala Asp Ile
 165 170 175
 Tyr Ile Pro Thr Leu Glu Glu Ile Lys Arg Thr Leu Gln Leu Ala Lys
 180 185 190
 10 Asp Tyr Ser Glu Asn Val Tyr Phe Ile Tyr Arg Ile Ala Leu Glu Ser
 195 200 205
 Gly Val Arg Leu Ser Glu Ile Leu Lys Val Leu Lys Glu Pro Glu Arg
 210 215 220
 15 Asp Ile Cys Gly Asn Asp Val Cys Tyr Tyr Pro Leu Ser Trp Thr Arg
 225 230 235 240
 20 Gly Tyr Lys Gly Val Phe Tyr Val Phe His Ile Thr Pro Leu Lys Arg
 245 250 255
 Val Glu Val Thr Lys Trp Ala Ile Ala Asp Phe Glu Arg Arg His Lys
 260 265 270
 25 Asp Ala Ile Ala Ile Lys Tyr Phe Arg Lys Phe Val Ala Ser Lys Met
 275 280 285
 Ala Glu Leu Ser Val Pro Leu Asp Ile Ile Asp Phe Ile Gln Gly Arg
 290 295 300
 30 Lys Pro Thr Arg Val Leu Thr Gln His Tyr Val Ser Leu Phe Gly Ile
 305 310 315 320
 35 Ala Lys Glu Gln Tyr Lys Lys Tyr Ala Glu Trp Leu Lys Gly Val
 325 330 335
 40 <210> 66
 <211> 1441
 <212> DNA
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 45 <220>
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 coding for fusion protein NLS-XisA
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 <400> 66
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 caa caa gcc ttt gca gac tta gag cca ctt tca tct acc gac ggc agt 96
 60 Gln Gln Ala Phe Ala Asp Leu Glu Pro Leu Ser Ser Thr Asp Gly Ser
 20 25 30
 ttt ctc ggc tca agt ctg caa gca cag cag caa aga gaa cac atg aga 144
 Phe Leu Gly Ser Ser Leu Gln Ala Gln Gln Gln Arg Glu His Met Arg
 35 40 45
 65 aca aaa gta cta caa gac cta gac aag gta aat ctg cgt ttg aag tct 192
 Thr Lys Val Leu Gln Asp Leu Asp Lys Val Asn Leu Arg Leu Lys Ser

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5	gca aag acg aaa gtc tca gtt cga gaa tct aac gga agt ctg caa tta Ala Lys Thr Lys Val Ser Val Arg Glu Ser Asn Gly Ser Leu Gln Leu 65 70 75 80	240				
10	cga gca acg tta cca att aaa cct gga gat aag gac acc aac ggt aca Arg Ala Thr Leu Pro Ile Lys Pro Gly Asp Lys Asp Thr Asn Gly Thr 85 90 95	288				
15	ggc aga aag caa tac aat ctc agc ttg aat atc cct gca aac ttg gat Gly Arg Lys Gln Tyr Asn Leu Ser Leu Asn Ile Pro Ala Asn Leu Asp 100 105 110	336				
20	gga ctg aag acg gct gag gaa gaa gct tat gaa tta ggt aaa tta atc Gly Leu Lys Thr Ala Glu Glu Glu Ala Tyr Glu Leu Gly Lys Leu Ile 115 120 125	384				
25	gct cgg aaa acc ttt gaa tgg aat gat aaa tat tta ggc aaa gaa gcc Ala Arg Lys Thr Phe Glu Trp Asn Asp Lys Tyr Leu Gly Lys Glu Ala 130 135 140	432				
30	act aaa aaa gat tca caa aca ata ggt gat tta cta gaa aaa ttt gca Thr Lys Lys Asp Ser Gln Thr Ile Gly Asp Leu Leu Glu Lys Phe Ala 145 150 155 160	480				
35	gaa gag tat ttt aaa acc cat aaa cgc acc act aaa agc gaa cat acc Glu Glu Tyr Phe Lys Thr His Lys Arg Thr Thr Lys Ser Glu His Thr 165 170 175	528				
40	ttt ttt tac tat ttt tcc cgc acc caa cga tat acc aat tcc aaa gat Phe Phe Tyr Tyr Phe Ser Arg Thr Gln Arg Tyr Thr Asn Ser Lys Asp 180 185 190	576				
45	tta gca acg gcg gaa aat ctc atc aat tca att gag caa atc gat aaa Leu Ala Thr Ala Glu Asn Leu Ile Asn Ser Ile Glu Gln Ile Asp Lys 195 200 205	624				
50	gaa tgg gcg aga tat aat gcc gcc aga gcc ata tca gct ttt tgc ata Glu Trp Ala Arg Tyr Asn Ala Ala Arg Ala Ile Ser Ala Phe Cys Ile 210 215 220	672				
55	aca ttc aat ata gaa att gat ttg tcc cag tat tcc aaa atg cct gat Thr Phe Asn Ile Glu Ile Asp Leu Ser Gln Tyr Ser Lys Met Pro Asp 225 230 235 240	720				
60	cgc aat tcg cgc aac atc ccc aca gat gca gaa ata cta tca gga att Arg Asn Ser Arg Asn Ile Pro Thr Asp Ala Glu Ile Leu Ser Gly Ile 245 250 255	768				
65	acc aaa ttt gaa gac tat cta gtt acc aga gga aat caa gtt aat gaa Thr Lys Phe Glu Asp Tyr Leu Val Thr Arg Gly Asn Gln Val Asn Glu 260 265 270	816				
70	gat gta aaa gat agc tgg caa ctt tgg cgc tgg aca tat gga atg tta Asp Val Lys Asp Ser Trp Gln Leu Trp Arg Trp Thr Tyr Gly Met Leu 275 280 285	864				
75	gca gtt ttt ggt tta cgc ccc agg gaa att ttt att aac cct aat att Ala Val Phe Gly Leu Arg Pro Arg Glu Ile Phe Ile Asn Pro Asn Ile 290 295 300	912				
80	gat tgg tgg tta agc aaa gag aat ata gac ctc aca tgg aaa gta gac Asp Trp Trp Leu Ser Lys Glu Asn Ile Asp Leu Thr Trp Lys Val Asp 305 310 315 320	960				
85	aaa gaa tgt aaa act ggt gaa aga caa gca tta ccc tta cat aaa gaa	1008				

Lys Glu Cys Lys Thr Gly Glu Arg Gln Ala Leu Pro Leu His Lys Glu
 325 330 335
 5 tgg att gat gag ttt gat tta aga aat ccg aaa tat tta gaa atg ctg 1056
 Trp Ile Asp Glu Phe Asp Leu Arg Asn Pro Lys Tyr Leu Glu Met Leu
 340 345 350
 10 gca aca gca att agt aaa aaa gat aaa aca aat cat gct gaa ata aca 1104
 Ala Thr Ala Ile Ser Lys Lys Asp Lys Thr Asn His Ala Glu Ile Thr
 355 360 365
 15 gcc tta act cag cgt att agt tgg tgg ttt cgg aaa gtc gaa tta gat 1152
 Ala Leu Thr Gln Arg Ile Ser Trp Trp Phe Arg Lys Val Glu Leu Asp
 370 375 380
 20 ttt aaa ccc tat gat tta cgt cac gcc tgg gca atc aga gcg cat att 1200
 Phe Lys Pro Tyr Asp Leu Arg His Ala Trp Ala Ile Arg Ala His Ile
 385 390 395 400
 25 tta ggc ata cca atc aaa gcg gcg gct gat aat ttg ggg cat agt atg 1248
 Leu Gly Ile Pro Ile Lys Ala Ala Ala Asp Asn Leu Gly His Ser Met
 405 410 415
 30 cag gtt cat aca caa acc tat cag cgc tgg ttc tcg cta gat atg cgg 1296
 Gln Val His Thr Gln Thr Tyr Gln Arg Trp Phe Ser Leu Asp Met Arg
 420 425 430
 35 aag tta gcg att aat cag gct ttg act aag agg aat gaa ttt gag gtg 1344
 Lys Leu Ala Ile Asn Gln Ala Leu Thr Lys Arg Asn Glu Phe Glu Val
 435 440 445
 40 att agg gag gag aat gct aaa ttg cag ata gaa aat gaa agg ttg agg 1392
 Ile Arg Glu Glu Asn Ala Lys Leu Gln Ile Glu Asn Glu Arg Leu Arg
 450 455 460
 45 atg gaa att gag aag tta aag atg gaa ata gct tat aag aat agt tgag 1441
 Met Glu Ile Glu Lys Leu Lys Met Glu Ile Ala Tyr Lys Asn Ser
 465 470 475
 50 <210> 67
 <211> 479
 <212> PRT
 <213> Artificial Sequence
 <223> Description of Artificial Sequence: DNA sequence
 coding for fusion protein NLS-XisA
 <400> 67
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 1 5 10 15
 Gln Gln Ala Phe Ala Asp Leu Glu Pro Leu Ser Ser Thr Asp Gly Ser
 20 25 30
 55 Phe Leu Gly Ser Ser Leu Gln Ala Gln Gln Gln Arg Glu His Met Arg
 35 40 45
 60 Thr Lys Val Leu Gln Asp Leu Asp Lys Val Asn Leu Arg Leu Lys Ser
 50 55 60
 Ala Lys Thr Lys Val Ser Val Arg Glu Ser Asn Gly Ser Leu Gln Leu
 65 70 75 80
 65 Arg Ala Thr Leu Pro Ile Lys Pro Gly Asp Lys Asp Thr Asn Gly Thr
 85 90 95
 Gly Arg Lys Gln Tyr Asn Leu Ser Leu Asn Ile Pro Ala Asn Leu Asp

	100	105	110	
	Gly Leu Lys Thr Ala Glu Glu Glu Ala Tyr Glu Leu Gly Lys Leu Ile			
5	115	120	125	
	Ala Arg Lys Thr Phe Glu Trp Asn Asp Lys Tyr Leu Gly Lys Glu Ala			
	130	135	140	
10	Thr Lys Lys Asp Ser Gln Thr Ile Gly Asp Leu Leu Glu Lys Phe Ala			
	145	150	155	160
	Glu Glu Tyr Phe Lys Thr His Lys Arg Thr Thr Lys Ser Glu His Thr			
	165	170	175	
15	Phe Phe Tyr Tyr Phe Ser Arg Thr Gln Arg Tyr Thr Asn Ser Lys Asp			
	180	185	190	
	Leu Ala Thr Ala Glu Asn Leu Ile Asn Ser Ile Glu Gln Ile Asp Lys			
20	195	200	205	
	Glu Trp Ala Arg Tyr Asn Ala Ala Arg Ala Ile Ser Ala Phe Cys Ile			
	210	215	220	
25	Thr Phe Asn Ile Glu Ile Asp Leu Ser Gln Tyr Ser Lys Met Pro Asp			
	225	230	235	240
	Arg Asn Ser Arg Asn Ile Pro Thr Asp Ala Glu Ile Leu Ser Gly Ile			
	245	250	255	
30	Thr Lys Phe Glu Asp Tyr Leu Val Thr Arg Gly Asn Gln Val Asn Glu			
	260	265	270	
	Asp Val Lys Asp Ser Trp Gln Leu Trp Arg Trp Thr Tyr Gly Met Leu			
35	275	280	285	
	Ala Val Phe Gly Leu Arg Pro Arg Glu Ile Phe Ile Asn Pro Asn Ile			
	290	295	300	
40	Asp Trp Trp Leu Ser Lys Glu Asn Ile Asp Leu Thr Trp Lys Val Asp			
	305	310	315	320
	Lys Glu Cys Lys Thr Gly Glu Arg Gln Ala Leu Pro Leu His Lys Glu			
	325	330	335	
45	Trp Ile Asp Glu Phe Asp Leu Arg Asn Pro Lys Tyr Leu Glu Met Leu			
	340	345	350	
	Ala Thr Ala Ile Ser Lys Lys Asp Lys Thr Asn His Ala Glu Ile Thr			
50	355	360	365	
	Ala Leu Thr Gln Arg Ile Ser Trp Trp Phe Arg Lys Val Glu Leu Asp			
	370	375	380	
55	Phe Lys Pro Tyr Asp Leu Arg His Ala Trp Ala Ile Arg Ala His Ile			
	385	390	395	400
	Leu Gly Ile Pro Ile Lys Ala Ala Ala Asp Asn Leu Gly His Ser Met			
	405	410	415	
60	Gln Val His Thr Gln Thr Tyr Gln Arg Trp Phe Ser Leu Asp Met Arg			
	420	425	430	
	Lys Leu Ala Ile Asn Gln Ala Leu Thr Lys Arg Asn Glu Phe Glu Val			
65	435	440	445	
	Ile Arg Glu Glu Asn Ala Lys Leu Gln Ile Glu Asn Glu Arg Leu Arg			
	450	455	460	

Met Glu Ile Glu Lys Leu Lys Met Glu Ile Ala Tyr Lys Asn Ser
 465 470 475

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<210> 68
 <211> 1029
 <212> DNA

10 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: DNA sequence
 coding for fusion protein NLS-Ssv

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<220>
 <221> CDS
 <222> (1)..(1026)

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 1 5 10 15

5

tac ggg gat tat att tta cgc gag agg aaa ggg cgg tat tat gtt tac 96
 Tyr Gly Asp Tyr Ile Leu Arg Glu Arg Lys Gly Arg Tyr Tyr Val Tyr
 20 25 30

10

aag cta gag tat gaa aac ggt gag gta aaa gag cgt tac gtg ggt cct 144
 Lys Leu Glu Tyr Glu Asn Gly Glu Val Lys Glu Arg Tyr Val Gly Pro
 35 40 45

35

tta gct gac gtc gtt gaa tca tat cta aaa atg aaa tta ggg gtc gta 192
 Leu Ala Asp Val Val Glu Ser Tyr Leu Lys Met Lys Leu Gly Val Val
 50 55 60

40

ggg gat act ccc cta caa gcg gat ccc ccc ggt ttc gag ccc ggg aca 240
 Gly Asp Thr Pro Leu Gln Ala Asp Pro Pro Gly Phe Glu Pro Gly Thr
 65 70 75 80

agc gga agc ggt ggt gga aaa gag gga act gaa cga cgt aaa ata gcg 288
 Ser Gly Ser Gly Gly Gly Lys Glu Gly Thr Glu Arg Arg Lys Ile Ala
 85 90 95

45

ttg gtt gcc aat ttg cgc caa tac gcg acg gac ggc aac ata aag gcg 336
 Leu Val Ala Asn Leu Arg Gln Tyr Ala Thr Asp Gly Asn Ile Lys Ala
 100 105 110

50

ttc tac aac tat ctc atg aac gaa agg ggg ata agc gaa aaa act gca 384
 Phe Tyr Asn Tyr Leu Met Asn Glu Arg Gly Ile Ser Glu Lys Thr Ala
 115 120 125

55

aag gac tac atc aat gct ata tca aag ccg tat aaa gag acg aga gac 432
 Lys Asp Tyr Ile Asn Ala Ile Ser Lys Pro Tyr Lys Glu Thr Arg Asp
 130 135 140

60

gca cag aag gct tac cga ctc ttt gca cgt ttc tta gcg tca cgc aat 480
 Ala Gln Lys Ala Tyr Arg Leu Phe Ala Arg Phe Leu Ala Ser Arg Asn
 145 150 155 160

atc ata cat gat gaa ttt gcg gat aaa ata ttg aaa gcg gta aag gtg 528
 Ile Ile His Asp Glu Phe Ala Asp Lys Ile Leu Lys Ala Val Lys Val
 165 170 175

65

aag aag gcg aac gct gat atc tac att cca acg ttg gaa gag ata aaa 576
 Lys Lys Ala Asn Ala Asp Ile Tyr Ile Pro Thr Leu Glu Glu Ile Lys
 180 185 190

1008

Leu Val Ala Asn Leu Arg Gln Tyr Ala Thr Asp Gly Asn Ile Lys Ala
 100 105 110
 5 Phe Tyr Asn Tyr Leu Met Asn Glu Arg Gly Ile Ser Glu Lys Thr Ala
 115 120 125
 Lys Asp Tyr Ile Asn Ala Ile Ser Lys Pro Tyr Lys Glu Thr Arg Asp
 130 135 140
 10 Ala Gln Lys Ala Tyr Arg Leu Phe Ala Arg Phe Leu Ala Ser Arg Asn
 145 150 155 160
 15 Ile Ile His Asp Glu Phe Ala Asp Lys Ile Leu Lys Ala Val Lys Val
 165 170 175
 Lys Lys Ala Asn Ala Asp Ile Tyr Ile Pro Thr Leu Glu Glu Ile Lys
 180 185 190
 20 Arg Thr Leu Gln Leu Ala Lys Asp Tyr Ser Glu Asn Val Tyr Phe Ile
 195 200 205
 Tyr Arg Ile Ala Leu Glu Ser Gly Val Arg Leu Ser Glu Ile Leu Lys
 210 215 220
 25 Val Leu Lys Glu Pro Glu Arg Asp Ile Cys Gly Asn Asp Val Cys Tyr
 225 230 235 240
 Tyr Pro Leu Ser Trp Thr Arg Gly Tyr Lys Gly Val Phe Tyr Val Phe
 245 250 255
 His Ile Thr Pro Leu Lys Arg Val Glu Val Thr Lys Trp Ala Ile Ala
 260 265 270
 Asp Phe Glu Arg Arg His Lys Asp Ala Ile Ala Ile Lys Tyr Phe Arg
 275 280 285
 40 Lys Phe Val Ala Ser Lys Met Ala Glu Leu Ser Val Pro Leu Asp Ile
 290 295 300
 Ile Asp Phe Ile Gln Gly Arg Lys Pro Thr Arg Val Leu Thr Gln His
 305 310 315 320
 45 Tyr Val Ser Leu Phe Gly Ile Ala Lys Glu Gln Tyr Lys Lys Tyr Ala
 325 330 335
 Glu Trp Leu Lys Gly Val
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 <211> 3908
 <212> DNA
 55 <213> Artificial Sequence
 <220>
 <223> Description of Artificial Sequence: vector
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 cgagataggg ttgagtgttg ttccagtttg gaacaagagt ccactattaa agaacgtgga 180
 ctccaacgtc aaagggcgaa aaaccgtcta tcagggcgat ggcccaactac gtgaaccatc 240
 accctaataca agtttttttg ggtcgaggtg ccgtaaagca ctaaatcgga accctaaagg 300
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<210> 71
<211> 3927
<212> DNA
<213> Artificial Sequence
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65.

<220>

<223> Description of Artificial Sequence: vector
pBS-SSV4

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 cgagataggg ttgagtgttg ttccagtttg gaacaagagt ccactattaa agaacgtgga 180
 ctccaacgtc aaagggcgaa aaaccgtcta tcagggcgat ggcccactac gtgaaccatc 240
 10 accctaataca agtttttttg ggtcgaggtg ccgtaaagca ctaaatcgga accctaaagg 300
 gagccccga ttttagagctt gacggggaaa gccggcgaac gtggcgagaa aggaagggaa 360
 gaaagcgaaa ggagcgggag ctagggcgct ggcaagtgtg gcggtcacgc tgcgcgtaac 420
 caccacaccc gccgcgctta atgcgcgctt acagggcgcg tcccatcgc cattcaggct 480
 gcgcaactgt tgggaagggc gatcggtgcg ggccctcttc ctattacgcc agctggcgaa 540
 15 aggggatgtg gctgcaaggc gattaagtgt ggtaacgcca gggttttccc agtcacgacg 600
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 ccgcggtggc ggccgcacca tgcccaagaa gaagaggaag gtgacgaaag ataagacgcg 720
 ttataaatac ggggattata ttttacgcga gaggaaaggg cggattatag tttaacaagt 780
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<211> 3351

<212> DNA

10 <213> Artificial Sequence

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<223> Description of Artificial Sequence: vector
 PBS-SSVs

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 cggggagagg cggtttgcgt attgggcgct ctcccgcttc ctgcgtcact gactcgtctg 720
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<211> 5730

10 <212> DNA

<213> Artificial Sequence

<220>

15 <223> Description of Artificial Sequence: vector
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 Val Phe Thr Lys Asn Lys Ile Asp Phe Ile Ser Leu Asn Glu Ser Ile
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 Asp Thr Ser Ser Ala Met Gly Ser Leu Phe Leu Thr Ile Leu Ser Ala
 115 120 125

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 Ile Asn Glu Phe Glu Arg Glu Asn Ile Lys Glu Arg Met Thr Met Gly
 130 135 140

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	Lys Leu Gly Arg Ala Lys Ser Gly Lys Ser Met Met Trp Thr Lys Thr	
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5	gct ttt ggg tat tac cac aac aga aag aca ggt ata tta gaa att gtt	528
	Ala Phe Gly Tyr Tyr His Asn Arg Lys Thr Gly Ile Leu Glu Ile Val	
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	Pro Leu Gln Ala Thr Ile Val Glu Gln Ile Phe Thr Asp Tyr Leu Ser	
	180 185 190	
15	gga ata tca ctt aca aaa tta aga gat aaa ctc aat gaa tct gga cac	624
	Gly Ile Ser Leu Thr Lys Leu Arg Asp Lys Leu Asn Glu Ser Gly His	
	195 200 205	
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	Ile Gly Lys Asp Ile Pro Trp Ser Tyr Arg Thr Leu Arg Gln Thr Leu	
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	gat aat cca gtt tac tgt ggt tat atc aaa ttt aag gac agc cta ttt	720
	Asp Asn Pro Val Tyr Cys Gly Tyr Ile Lys Phe Lys Asp Ser Leu Phe	
	225 230 235 240	
	gaa ggt atg cac aaa cca att atc cct tat gag act tat tta aaa gtt	768
	Glu Gly Met His Lys Pro Ile Ile Pro Tyr Glu Thr Tyr Leu Lys Val	
	245 250 255	
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	Asn Pro Arg Pro Phe Gln Ala Lys Tyr Met Leu Ser Gly Met Ala Arg	
	275 280 285	
40	tgc ggt tac tgt gga gca cct tta aaa att gtt ctt ggc cac aaa aga	912
	Cys Gly Tyr Cys Gly Ala Pro Leu Lys Ile Val Leu Gly His Lys Arg	
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	Lys Asp Gly Ser Arg Thr Met Lys Tyr His Cys Ala Asn Arg Phe Pro	
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45	cga aaa aca aaa gga att aca gta tat aat gac aat aaa aag tgt gat	1008
	Arg Lys Thr Lys Gly Ile Thr Val Tyr Asn Asp Asn Lys Lys Cys Asp	
	325 330 335	
50	tca gga act tat gat tta agt aat tta gaa aat act gtt att gac aac	1056
	Ser Gly Thr Tyr Asp Leu Ser Asn Leu Glu Asn Thr Val Ile Asp Asn	
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	Leu Ile Gly Phe Gln Glu Asn Asn Asp Ser Leu Leu Lys Ile Ile Asn	
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	Asp Phe Ile Thr Met Asp Glu Leu Lys Asp Arg Thr Asp Ser Leu Gln	
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 35 40 45
 Gly Phe Ser Gly Ala Lys Leu Glu Arg Pro Ala Met Gln Arg Leu Ile
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 40 Asn Asp Ile Glu Asn Lys Ala Phe Asp Thr Val Leu Val Tyr Lys Leu
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 45 Asp Arg Leu Ser Arg Ser Val Arg Asp Thr Leu Tyr Leu Val Lys Asp
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 55 Lys Leu Gly Arg Ala Lys Ser Gly Lys Ser Met Met Trp Thr Lys Thr
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 60 Ala Phe Gly Tyr Tyr His Asn Arg Lys Thr Gly Ile Leu Glu Ile Val
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 Pro Leu Gln Ala Thr Ile Val Glu Gln Ile Phe Thr Asp Tyr Leu Ser
 180 185 190
 65 Gly Ile Ser Leu Thr Lys Leu Arg Asp Lys Leu Asn Glu Ser Gly His
 195 200 205

Ile Gly Lys Asp Ile Pro Trp Ser Tyr Arg Thr Leu Arg Gln Thr Leu
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 5 Asp Asn Pro Val Tyr Cys Gly Tyr Ile Lys Phe Lys Asp Ser Leu Phe
 225 230 235 240
 Glu Gly Met His Lys Pro Ile Ile Pro Tyr Glu Thr Tyr Leu Lys Val
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 10 Gln Lys Glu Leu Glu Glu Arg Gln Gln Gln Thr Tyr Glu Arg Asn Asn
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 Arg Lys Thr Lys Gly Ile Thr Val Tyr Asn Asp Asn Lys Lys Cys Asp
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 Ser Gly Thr Tyr Asp Leu Ser Asn Leu Glu Asn Thr Val Ile Asp Asn
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 Lys Phe Gln Leu Ala
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